

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 27, 2003, 16:04:16 ; Search time 17 Seconds  
(without alignments)  
655.958 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFFS.....PATERCVLSRMSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata1/1/aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata1/1/aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata1/1/aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata1/1/aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata1/1/aa/6C\_COMB.pep.\*  
6: /cgn2\_6/ptodata1/1/aa/6D\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result- No.	Score	Query Match	Length	ID	Description
1	1799	90.3	373	4	US-09-724-864-43
2	1021	51.3	368	1	US-08-303-238-3
3	1021	51.3	368	4	US-08-458-834-3
4	1020	51.2	368	6	5340934-2
5	963.5	48.4	359	1	US-08-303-238-4
6	963.5	48.4	359	4	US-08-458-834-4
7	949	47.6	342	1	US-08-272-919-2
8	949	47.6	342	1	US-08-619-916-2
9	949	47.6	342	5	PCI-US95-08542-2
10	947	47.5	333	1	US-08-442-063A-27
11	907	45.5	353	6	5340934-4
12	847	42.5	307	1	US-08-442-063A-48
13	776	39.0	282	1	US-08-442-063A-45
14	616	30.9	236	1	US-08-442-063A-42
15	493	24.7	188	1	US-08-442-063A-39
16	384.5	19.3	141	1	US-08-442-063A-36
17	342.5	17.2	375	1	US-08-303-238-2
18	342.5	17.2	375	4	US-08-458-834-2
19	336	16.9	1525	3	US-09-191-647-2
20	336	16.9	1525	4	US-09-540-245A-2
21	336	16.9	1525	4	US-09-540-153-2
22	334.5	16.8	649	4	US-09-188-930-305
23	318	16.0	376	1	US-08-303-238-1
24	318	16.0	376	4	US-08-458-834-1
25	316	15.9	1480	3	US-09-191-647-7
26	316	15.9	1480	4	US-09-540-245A-7
27	316	15.9	1480	4	US-09-540-153-7

28	316	15.9	1480	5	PCT-US91-09055-2	Sequence 2, Appli
29	313	15.7	1480	4	US-09-182-024A-5	Sequence 5, Appli
30	309	15.5	1523	4	US-09-182-024A-2	Sequence 2, Appli
31	296	14.9	1091	3	US-08-986-485-5	Sequence 5, Appli
32	272	13.7	603	1	US-08-190-802A-50	Sequence 50, Appli
33	272	13.7	603	4	US-08-477-346-50	Sequence 50, Appli
34	272	13.7	603	4	US-08-473-089-50	Sequence 50, Appli
35	272	13.7	603	4	US-08-487-072A-50	Sequence 50, Appli
36	262	13.2	708	4	US-09-131-648-2	Sequence 2, Appli
37	259.5	13.0	1101	3	US-08-986-485-2	Sequence 2, Appli
38	256.5	12.9	96	1	US-08-442-063A-33	Sequence 33, Appli
39	254	12.8	353	3	US-08-986-485-6	Sequence 6, Appli
40	246	12.3	605	1	US-08-190-802A-49	Sequence 49, Appli
41	246	12.3	605	4	US-08-477-346-49	Sequence 49, Appli
42	246	12.3	605	4	US-08-473-089-49	Sequence 49, Appli
43	246	12.3	605	4	US-08-487-072A-49	Sequence 49, Appli
44	241	12.1	605	4	US-09-063-950-5	Sequence 5, Appli
45	241	12.1	673	4	US-09-063-950-2	Sequence 2, Appli
46	239	12.0	180	3	US-08-986-485-8	Sequence 8, Appli
47	236	11.8	440	3	US-08-985-335-3	Sequence 3, Appli
48	236	11.8	440	4	US-09-410-372-3	Sequence 3, Appli
49	222	11.1	224	5	PCT-US91-09055-4	Sequence 4, Appli
50	212.5	10.7	298	4	US-09-232-160-17	Sequence 17, Appli
51	206	10.3	222	5	PCT-US91-09055-3	Sequence 3, Appli
52	206	10.3	231	3	US-08-986-485-7	Sequence 7, Appli
53	205	10.3	313	3	US-08-985-335-8	Sequence 8, Appli
54	205	10.3	313	4	US-09-410-372-8	Sequence 8, Appli
55	199.5	10.0	560	3	US-08-592-500-2	Sequence 2, Appli
56	199.5	10.0	560	3	US-08-195-006-2	Sequence 2, Appli
57	199.5	10.0	560	4	US-09-063-950-4	Sequence 4, Appli
58	199.5	10.0	560	5	PCT-US94-07644A-2	Sequence 2, Appli
59	195	9.8	610	1	US-07-821-717B-6	Sequence 6, Appli
60	195	9.8	610	1	US-08-119-262B-6	Sequence 6, Appli
61	195	9.8	610	1	US-08-135-929A-11	Sequence 11, Appli
62	195	9.8	610	1	US-08-234-265A-11	Sequence 11, Appli
63	194	9.7	320	1	US-07-613-083B-1	Sequence 1, Appli
64	184.5	9.3	196	5	PCT-US91-09055-6	Sequence 6, Appli
65	181	9.1	746	5	PCT-US95-10509-2	Sequence 2, Appli
66	177	8.9	196	5	PCT-US91-09055-5	Sequence 5, Appli
67	175.5	8.8	661	1	US-08-514-014-4	Sequence 4, Appli
68	175.5	8.8	661	2	US-08-833-823-4	Sequence 4, Appli
69	175	8.8	1112	4	US-09-353-585-2	Sequence 2, Appli
70	173	8.7	55	1	US-08-442-063A-57	Sequence 57, Appli
71	172	8.6	1112	4	US-09-353-585-3	Sequence 3, Appli
72	170.5	8.6	110	4	US-09-188-930-124	Sequence 124, App
73	170.5	8.6	806	4	US-08-945-983-2	Sequence 2, Appli
74	169	8.5	1016	4	US-09-180-439-8	Sequence 8, Appli
75	168	8.4	968	4	US-09-180-439-3	Sequence 3, Appli
76	168	8.4	968	4	US-09-180-439-4	Sequence 4, Appli
77	166.5	8.4	134	3	US-09-191-647-12	Sequence 12, Appli
78	166.5	8.4	134	4	US-09-540-245A-12	Sequence 12, Appli
79	166.5	8.4	134	4	US-09-540-153-12	Sequence 12, Appli
80	163	8.2	55	1	US-08-442-063A-60	Sequence 60, Appli
81	163	8.2	799	4	US-09-180-439-6	Sequence 6, Appli
82	161.5	8.1	1012	2	US-08-475-891A-4	Sequence 4, Appli
83	161.5	8.1	1025	2	US-08-567-375-4	Sequence 4, Appli
84	161.5	8.1	1025	2	US-08-587-680A-4	Sequence 4, Appli
85	161	8.1	692	4	US-07-757-342D-6	Sequence 6, Appli
86	160	8.0	863	2	US-08-666-271-2	Sequence 2, Appli
87	159	8.0	735	3	US-09-191-647-9	Sequence 9, Appli
88	159	8.0	735	4	US-09-540-245A-9	Sequence 9, Appli
89	159	8.0	735	4	US-09-540-153-9	Sequence 9, Appli
90	156	7.8	999	2	US-08-473-553A-5	Sequence 5, Appli
91	150	7.5	947	4	US-09-228-986-73	Sequence 73, Appli
92	149	7.5	1023	2	US-08-475-891A-2	Sequence 2, Appli
93	149	7.5	1023	2	US-08-567-375-2	Sequence 2, Appli
94	149	7.5	1023	2	US-08-587-680A-2	Sequence 2, Appli
95	147.5	7.4	910	4	US-09-228-986-72	Sequence 72, Appli
96	145.5	7.3	1196	4	US-08-881-706-2	Sequence 2, Appli
97	143.5	7.2	155	3	US-09-191-647-8	Sequence 8, Appli
98	143.5	7.2	155	4	US-09-540-245A-8	Sequence 8, Appli
99	143.5	7.2	155	4	US-09-540-153-8	Sequence 8, Appli
100	142.5	7.2	105	3	US-09-191-647-3	Sequence 3, Appli

101	142.5	7.2	105	4	US-09-540-245A-3	Sequence 3, Appli	174	100.5	5.0	456	2	US-08-795-395-2	Sequence 2, Appli
102	142.5	7.2	105	4	US-09-540-153-3	Sequence 3, Appli	175	99	5.0	1366	4	US-09-004-838-22	Sequence 22, Appli
103	140.5	7.1	390	3	US-08-460-576-2	Sequence 2, Appli	176	99	5.0	1890	4	US-09-004-838-88	Sequence 88, Appli
104	140.5	7.1	695	3	US-08-487-886-2	Sequence 2, Appli	177	98.5	4.9	764	4	US-07-757-342D-5	Sequence 5, Appli
105	140.5	7.1	695	3	US-08-482-855-2	Sequence 2, Appli	178	98.5	4.9	764	4	US-07-741-345A-59	Sequence 59, Appli
106	140.5	7.1	695	4	US-08-474-986-2	GENERAL INFORMA	179	98.5	4.9	764	4	US-07-741-453A-61	Sequence 61, Appli
107	135	6.8	968	4	US-09-228-986-76	Sequence 76, Appli	180	98	4.9	418	1	US-08-224-930-4	Sequence 4, Appli
108	134.5	6.8	644	2	US-08-866-757-2	Sequence 2, Appli	181	98	4.9	418	4	US-08-908-436-6	Sequence 6, Appli
109	134.5	6.8	644	4	US-09-153-593-2	Sequence 2, Appli	182	98	4.9	418	4	US-09-561-756-18	Sequence 18, Appli
110	128	6.4	740	1	US-08-257-073-5	Sequence 5, Appli	183	98	4.9	418	4	US-09-227-721-18	Sequence 18, Appli
111	125.5	6.3	342	1	US-08-244-646-15	Sequence 15, Appli	184	98	4.9	795	4	US-07-741-453A-55	Sequence 55, Appli
112	125.5	6.3	342	1	US-08-592-936B-21	Sequence 21, Appli	185	98	4.9	847	1	US-08-286-305A-5	Sequence 5, Appli
113	125.5	6.3	342	2	US-09-111-573-21	Sequence 21, Appli	186	98	4.9	847	2	US-08-441-104A-5	Sequence 5, Appli
114	125.5	6.3	771	4	US-09-488-930-183	Sequence 183, App	187	98	4.9	847	2	US-08-440-816A-5	Sequence 5, Appli
115	125	6.3	674	4	US-07-757-342D-10	Sequence 10, Appli	188	98	4.9	847	4	US-09-417-381A-5	Sequence 5, Appli
116	122	6.1	699	4	US-07-757-342D-2	Sequence 2, Appli	189	98	4.9	966	4	US-09-207-359B-47	Sequence 47, Appli
117	122	6.1	523	2	US-08-473-553A-3	Sequence 3, Appli	190	97	4.9	36	1	US-08-240-712-35	Sequence 35, Appli
118	122	6.1	980	2	US-08-473-553A-6	Sequence 6, Appli	191	97	4.9	36	1	US-08-443-890-35	Sequence 35, Appli
119	122	6.1	985	2	US-08-473-553A-2	Sequence 2, Appli	192	97	4.9	611	4	US-07-757-342D-8	Sequence 8, Appli
120	121	6.1	596	4	US-09-752-165-2	Sequence 2, Appli	193	97	4.9	636	4	US-07-757-342D-7	Sequence 7, Appli
121	120.5	6.0	227	1	US-08-244-646-17	Sequence 17, Appli	194	97	4.9	758	4	US-09-134-001C-4588	Sequence 4588, Ap
122	118	5.9	700	4	US-07-757-342D-3	Sequence 3, Appli	195	97	4.9	821	1	US-08-339-578-2	Sequence 2, Appli
123	116.5	5.8	196	5	PCT-US91-09055-8	Sequence 8, Appli	196	96.5	4.8	47	1	US-08-442-063A-30	Sequence 30, Appli
124	115.5	5.8	690	4	US-09-228-986-69	Sequence 69, Appli	197	96	4.8	866	4	US-09-134-001C-4930	Sequence 4930, Ap
125	114	5.7	696	4	US-07-757-342D-4	Sequence 4, Appli	198	95.5	4.8	278	6	5340934-8	Patent No. 5340934
126	112.5	5.6	711	4	US-09-228-986-79	Sequence 79, Appli	199	95.5	4.8	920	3	US-08-930-996A-8	Sequence 8, Appli
127	112	5.6	327	1	US-08-238-163-4	Sequence 4, Appli	200	95	4.8	764	1	US-08-375-300-4	Sequence 4, Appli
128	110.5	5.5	456	2	US-08-910-731-4	Sequence 4, Appli	201	95	4.8	764	3	US-09-177-431-4	Sequence 4, Appli
129	110.5	5.5	456	2	US-08-910-731-8	Sequence 8, Appli	202	95	4.8	764	5	PCT-US95-16930-4	Sequence 4, Appli
130	110.5	5.5	456	2	US-08-795-395-4	Sequence 4, Appli	203	95	4.8	1089	1	US-08-375-300-2	Sequence 2, Appli
131	110	5.5	630	4	US-09-228-986-71	Sequence 71, Appli	204	95	4.8	1089	3	US-09-177-431-2	Sequence 2, Appli
132	109	5.5	428	1	US-08-190-802A-29	Sequence 29, Appli	205	95	4.8	1089	5	PCT-US95-16930-2	Sequence 2, Appli
133	109	5.5	428	4	US-08-477-346-29	Sequence 29, Appli	206	95	4.8	2285	4	US-09-308-375-2	Sequence 2, Appli
134	109	5.5	428	4	US-08-473-089-29	Sequence 29, Appli	207	94.5	4.7	366	3	US-08-746-883-6	Sequence 6, Appli
135	109	5.5	428	4	US-08-487-072A-29	Sequence 29, Appli	208	94.5	4.7	373	3	US-08-746-883-4	Sequence 4, Appli
136	109	5.5	850	1	US-08-286-305A-7	Sequence 7, Appli	209	94.5	4.7	1140	4	US-09-651-656-21	Sequence 21, Appli
137	109	5.5	850	2	US-08-441-104A-7	Sequence 7, Appli	210	94.5	4.7	1140	4	US-09-650-855-21	Sequence 21, Appli
138	109	5.5	850	2	US-08-440-816A-7	Sequence 7, Appli	211	94	4.7	311	4	US-09-134-001C-4235	Sequence 4235, Ap
139	109	5.5	850	4	US-09-417-381A-7	Sequence 7, Appli	212	94	4.7	477	2	US-08-359-705B-4	Sequence 4, Appli
140	108.5	5.4	1085	1	US-08-431-080-28	Sequence 28, Appli	213	94	4.7	477	2	US-08-286-846A-4	Sequence 4, Appli
141	108.5	5.4	1085	4	US-08-938-53A-28	Sequence 28, Appli	214	94	4.7	477	2	US-08-457-880A-4	Sequence 4, Appli
142	108.5	5.4	1085	4	US-09-345-29A-28	Sequence 28, Appli	215	94	4.7	477	3	US-08-444-622A-4	Sequence 4, Appli
143	107.5	5.4	707	4	US-09-228-986-80	Sequence 80, Appli	216	94	4.7	477	3	US-08-942-562-4	Sequence 4, Appli
144	107	5.4	903	4	US-09-228-986-78	Sequence 78, Appli	217	94	4.7	477	4	US-09-156-923-4	Sequence 4, Appli
145	106	5.3	825	1	US-07-912-952-2	Sequence 2, Appli	218	94	4.7	822	2	US-08-359-705B-2	Sequence 2, Appli
146	105	5.3	612	2	US-08-359-705B-8	Sequence 8, Appli	219	94	4.7	822	2	US-08-286-846A-2	Sequence 2, Appli
147	105	5.3	612	2	US-08-286-846A-8	Sequence 8, Appli	220	94	4.7	822	3	US-08-457-880A-2	Sequence 2, Appli
148	105	5.3	612	2	US-08-457-880A-8	Sequence 8, Appli	221	94	4.7	822	3	US-08-444-622A-2	Sequence 2, Appli
149	105	5.3	612	3	US-08-444-622A-8	Sequence 8, Appli	222	94	4.7	822	3	US-08-942-562-2	Sequence 2, Appli
150	105	5.3	612	3	US-08-942-562-8	Sequence 8, Appli	223	94	4.7	822	4	US-09-156-923-2	Sequence 2, Appli
151	105	5.3	839	2	US-09-156-923-8	Sequence 8, Appli	224	94	4.7	953	4	US-09-245-281-43	Sequence 43, Appli
152	105	5.3	839	2	US-08-359-705B-6	Sequence 6, Appli	225	94	4.7	953	4	US-09-207-359B-43	Sequence 43, Appli
153	105	5.3	839	2	US-08-286-846A-6	Sequence 6, Appli	226	93.5	4.7	1240	3	US-08-930-996A-4	Sequence 4, Appli
154	105	5.3	839	2	US-08-457-880A-6	Sequence 6, Appli	227	93	4.7	638	4	US-09-228-986-74	Sequence 74, Appli
155	105	5.3	839	3	US-08-444-622A-6	Sequence 6, Appli	228	93	4.7	739	4	US-09-022-983-2	Sequence 2, Appli
156	105	5.3	839	3	US-08-942-562-6	Sequence 6, Appli	229	93	4.7	907	3	US-08-930-996A-7	Sequence 7, Appli
157	105	5.3	839	4	US-09-156-923-6	Sequence 6, Appli	230	93	4.7	953	4	US-09-099-041A-8	Sequence 8, Appli
158	105	5.3	2391	2	US-08-446-855A-2	Sequence 2, Appli	231	93	4.7	953	4	US-09-245-281-8	Sequence 8, Appli
159	105	5.3	2391	3	US-09-150-741-2	Sequence 2, Appli	232	93	4.7	953	4	US-09-207-359B-8	Sequence 8, Appli
160	104	5.2	620	3	US-09-126-646-2	Sequence 2, Appli	233	93	4.7	4536	4	US-09-180-422B-27	Sequence 27, Appli
161	104	5.2	620	4	US-09-421-491-2	Sequence 2, Appli	234	92.5	4.6	1074	2	US-08-477-396A-4	Sequence 4, Appli
162	103.5	5.2	723	4	US-09-434-408-2	Sequence 2, Appli	235	92.5	4.6	1074	4	US-09-004-838-111	Sequence 111, App
163	103	5.2	330	1	US-08-238-163-2	Sequence 2, Appli	236	92.5	4.6	3135	1	US-08-323-170B-2	Sequence 2, Appli
164	102.5	5.1	764	4	US-07-741-453A-54	Sequence 54, Appli	237	92.5	4.6	3135	4	US-08-954-441-2	Sequence 2, Appli
165	102.5	5.1	764	4	US-07-741-453A-60	Sequence 60, Appli	238	92	4.6	1222	4	US-09-004-838-119	Sequence 119, App
166	102	5.1	277	4	US-07-741-453A-58	Sequence 58, Appli	239	91.5	4.6	1220	3	US-08-930-996A-2	Sequence 2, Appli
167	102	5.1	285	3	US-08-482-085B-20	Sequence 20, Appli	240	91	4.6	226	1	US-08-431-080-26	Sequence 26, Appli
168	102	5.1	461	2	US-08-910-731-6	Sequence 6, Appli	241	91	4.6	226	2	US-08-938-53A-26	Sequence 26, Appli
169	101	5.1	172	1	US-08-318-947A-11	Sequence 11, Appli	242	91	4.6	226	4	US-09-345-234-26	Sequence 26, Appli
170	101	5.1	172	2	US-08-795-203-11	Sequence 11, Appli	243	91	4.6	472	4	US-09-004-838-40	Sequence 40, Appli
171	101	5.1	172	3	US-09-358-580-14	Sequence 14, Appli	244	91	4.6	792	4	US-07-741-453A-56	Sequence 56, Appli
172	101	5.1	655	4	US-09-228-986-70	Sequence 70, Appli	245	91	4.6	1143	2	US-08-310-912A-108	Sequence 108, App
173	100.5	5.0	456	2	US-08-910-731-2	Sequence 2, Appli	246	91	4.6	1143	4	US-09-301-085-108	Sequence 108, App

247	91	4.6	1143	5	PCT-US95-04589-108	Sequence 108, App	320	85	4.3	853	4	US-08-913-880C-17	Sequence 17, Appl
248	91	4.6	1144	1	US-08-261-663A-2	Sequence 2, Appl	321	85	4.3	858	4	US-08-913-880C-16	Sequence 16, Appl
249	91	4.6	1144	1	US-08-261-663A-2	Sequence 4, Appl	322	85	4.3	860	4	US-08-913-880C-15	Sequence 15, Appl
250	91	4.6	1144	3	US-08-930-996A-9	Sequence 9, Appl	323	85	4.3	862	4	US-08-913-880C-14	Sequence 14, Appl
251	91	4.6	1144	3	US-09-357-206A-3	Sequence 3, Appl	324	85	4.3	865	4	US-08-913-880C-13	Sequence 13, Appl
252	91	4.6	1144	5	PCT-US95-0775A-2	Sequence 2, Appl	325	85	4.3	866	4	US-08-913-880C-12	Sequence 12, Appl
253	91	4.6	1144	5	PCT-US95-0775A-4	Sequence 4, Appl	326	85	4.3	874	4	US-08-913-880C-11	Sequence 11, Appl
254	91	4.6	1209	5	PCT-US95-04589-107	Sequence 107, App	327	85	4.3	875	4	US-08-913-880C-10	Sequence 10, Appl
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256	91	4.6	1258	4	US-09-301-085-107	Sequence 107, App	329	85	4.3	1388	4	US-09-572-191-2	Sequence 2, Appl
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259	91	4.6	1279	4	US-09-723-096-2	Sequence 2, Appl	332	85	4.3	1805	4	US-09-004-838-92	Sequence 92, Appl
260	91	4.6	1294	3	US-08-930-996A-10	Sequence 10, Appl	333	84.5	4.2	198	4	US-09-228-986-93	Sequence 93, Appl
261	90.5	4.5	162	1	US-07-879-685B-4	Sequence 4, Appl	334	84.5	4.2	295	2	US-08-679-765-5	Sequence 5, Appl
262	90.5	4.5	645	2	US-08-592-126-144	Sequence 144, App	335	84.5	4.2	295	2	US-09-196-525-5	Sequence 5, Appl
263	90.5	4.5	645	2	US-08-687-080-47	Sequence 47, Appl	336	84.5	4.2	295	4	US-09-318-317-5	Sequence 5, Appl
264	90.5	4.5	659	4	US-09-228-986-75	Sequence 75, Appl	337	84.5	4.2	295	4	US-09-177-165A-22	Sequence 22, Appl
265	90.5	4.5	1312	2	US-08-592-126-148	Sequence 148, App	338	84.5	4.2	359	4	US-09-198-955A-2	Sequence 2, Appl
266	90.5	4.5	1312	2	US-08-687-080-51	Sequence 51, Appl	339	84.5	4.2	359	4	US-09-395-858A-2	Sequence 2, Appl
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268	90	4.5	4302	3	US-08-658-136-5	Sequence 5, Appl	341	84.5	4.2	391	4	US-07-741-453A-2	Sequence 2, Appl
269	90	4.5	4302	4	US-09-052-469-8	Sequence 8, Appl	342	84.5	4.2	764	4	US-07-741-453A-29	Sequence 29, Appl
270	90	4.5	4339	4	US-09-052-469-6	Sequence 6, Appl	343	84.5	4.2	790	2	US-08-359-705B-9	Sequence 9, Appl
271	89.5	4.5	376	4	US-09-564-954-2	Sequence 2, Appl	344	84.5	4.2	790	2	US-08-286-846A-9	Sequence 9, Appl
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292	87.5	4.4	1727	2	US-08-477-451-10	Sequence 10, Appl	365	83.5	4.2	264	1	US-08-188-582-26	Sequence 26, Appl
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296	87	4.4	553	1	US-08-328-322-10	Sequence 10, Appl	369	83.5	4.2	460	3	US-08-960-507-17	Sequence 17, Appl
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Job time : 25 secs



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5	915	45.9	310	13	Q9DDZ8	petromyzon	
6	869.5	43.6	347	13	Q9DE00	petromyzon	
7	865.5	43.4	388	13	Q9DDZ9	petromyzon	
8	638.5	32.1	224	13	Q9DE01	brachydanio	
9	520	26.1	108	11	Q9CTL6	mus musculus	
10	397.5	20.0	699	4	Q94769	homo sapien	
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DT 01-JUN-2002	(TremBurel_21, Last annotation update)
DE	Bialycan-like protein 2.

GN BGL2.  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OX Petromyzontiformes; Petromyzontidae; Petromyzon.  
OC NCBI\_TaxID=7757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20496956; PubMed=11040287;  
RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;  
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";  
RL J. Mol. Evol. 51:363-373(2000).  
DR EMBL: AF247828; AAG40163.1; -.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR003591; LRR\_out.  
DR Pfam: PF01462; LRRNT; 1.  
DR SMART: SM00013; LRRNT; 1.  
DR SMART: SM00370; LRR; 4.  
DR SMART: SM00369; LRR\_TYP; 8.  
DR NON\_TER 1  
SQ SEQUENCE 410 AA; 44671 MW; 3EC96E490BFCCEFA CRC64;  
  
Query Match 46.0%; Score 917; DB 13; Length 410;  
Best Local Similarity 46.5%; Pred. No. 1.7e-57;  
Matches 192; Conservative 58; Mismatches 109; Indels 54; Gaps 7;  
  
QY 6 LLLFLAL-----CSAKPFPSHIALKNMMLKDMEDTDDDDDDDDDDDDDD 53  
Db 9 LLLVLCALSSPSSSVATATSSKPF-----AQROFFDFMADDAVFSGDD----- 55  
  
QY 54 SLPTREPR-----SHFFPDLP-----MCPFGCCYSRVVH 86  
Db 56 SVAPSTPKVGGDRSKATAGKOPGRGAATPKSLPPPPPPPPDASCFFGCQCSARVQ 115  
  
QY 87 CSOLGTSVPTNPFDTRMLDQNNKIKELKENDFGHLSLYGLIINNKKLTIHPKAPL 146  
Db 116 CSOLGLVSPQALPKDARLLDQNNKITEIKODDFKLNKLALYLVNLLISKVHPKAPA 175  
  
QY 147 TTKKRLRLYSHNQLSEIPLNPKSLAEHLRIHENKVKTKQDFTFGMNAHVLEMSANPL 206  
Db 176 PLSSLDKLYISHNQLTEVPGSPSSSLVELRIHENNIKKIPKDAFSCMKRLHALEMGGNPL 235  
  
QY 207 DNGIEPFAFEGV-TVFHRIAEAKTSVPKGLPPTLLEHLHDYNKISTVELEDFKRYKE 265  
Db 236 QSTGIEVGAFFGLRLVYRVSDSKLARIPKDLPLNSIQELHLEHNIQTALEQEDLIRYPL 295  
  
QY 266 LQRLGLGNKKTIDIEGSLANIPIRVREIHLNKKLKIIPSGLPKLYLOIIFLHNSIAR 325  
Db 296 IHRGLSYNQIKVONGSLSTCPHLRELHDSNVLTQVPPGLAFKHLQVYVYLSNKTAA 355  
  
QY 326 VGVNDFCTVPKMKKSLYSALSIFNNPVKYEMOPATFCVLSRMSVQLG-NF 377  
Db 356 VKSDDFCSKGSPKRVLYSGISLFDNPVNYWDVPPSAFRCVASRSVQFSQNF 408  
  
RESULT 5  
Q9DDZ8 PRELIMINARY; PRT; 310 AA.  
AC Q9DDZ8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE Biglycan-like protein 2 (Fragment).  
GN BGL2.  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OX Petromyzontiformes; Petromyzontidae; Petromyzon.  
OC NCBI\_TaxID=7757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20496956; PubMed=11040287;  
RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;

RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";  
RL J. Mol. Evol. 51:363-373(2000).  
DR EMBL: AF247827; AAG40162.1; -.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR003592; LRR\_Nterm.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003591; LRR\_typ.  
DR Pfam: PF00560; LRR; 7.  
DR Pfam: PF01462; LRRNT; 1.  
DR SMART: SM00370; LRR; 4.  
DR SMART: SM00013; LRRNT; 1.  
DR SMART: SM00369; LRR\_TYP; 8.  
DR NON\_TER 1  
SQ SEQUENCE 310 AA; 34572 MW; 6FB8E05B14339EF5 CRC64;  
  
Query Match 45.9%; Score 915; DB 13; Length 310;  
Best Local Similarity 56.2%; Pred. No. 1.7e-57;  
Matches 172; Conservative 51; Mismatches 81; Indels 2; Gaps 2;  
  
QY 74 CPGCCQYSRVVHCSDLGLTSVPTNPFDTRMLDQNNKIKELKENDFGHLSLYGLIIN 133  
Db 3 CPGCCQCSARVVOCSDLGLVSPQALPKDARLLDQNNKITEIKODDFKLNKLALYLV 62  
  
QY 134 NNKLRKTIHPKAPLTTKRLRLYSHNQLSEIPLNPKSLAEHLRIHENKVKTKQDTEKGM 193  
Db 63 NNLSKVHPKAPLSSLDKLYISHNQLTEVPGSPSSSLVELRIHENNIKKIPKDAFSGM 122  
  
QY 194 NALHVLEMSANPLDNNIEPFAFEGV-TVFHRIAEAKTSVPKGLPPTLLEHLHDYNKI 252  
Db 123 KRLHALEMGGNPLQSTGIEVGAFFGLRLVYRVSDSKLARIPKDLPLNSIQELHLEHNIQ 182  
  
QY 253 STVELEDFKRYKELORLGLGNKKTIDIEGSLANIPIRVREIHLNKKLKIIPSGLPKLY 312  
Db 193 TALEQEDLIRYPLIHRGLSYNQIKVONGSLSTCPHLRELHDSNVLTQVPPGLAFKHL 242  
  
QY 313 LOIIFLHNSIARVGVNDFCTVPKMKKSLYSALSIFNNPVKYEMOPATFCVLSRMSV 372  
Db 243 LQVYVYLSNKLAAVKSDDFCSGKSPKRVLYSGISLFDNPVNYWDVPPSAFRCVASRSV 302  
  
QY 373 QLG-NF 377  
Db 303 QFSQNF 308  
  
RESULT 6  
Q9DE00 PRELIMINARY; PRT; 347 AA.  
AC Q9DE00;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE Biglycan-like protein 1 (Fragment).  
GN BGLL.  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OX Petromyzontiformes; Petromyzontidae; Petromyzon.  
OC NCBI\_TaxID=7757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20496956; PubMed=11040287;  
RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;  
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";  
RL J. Mol. Evol. 51:363-373(2000).  
DR EMBL: AF247825; AAG40160.1; -.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR003592; LRR\_Nterm.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003591; LRR\_typ.  
DR Pfam: PF00560; LRR; 8.  
DR Pfam: PF01462; LRRNT; 1.  
DR SMART: SM00370; LRR; 4.  
DR SMART: SM00013; LRRNT; 1.  
DR SMART: SM00369; LRR\_TYP; 6.

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FT  NON_TER 1
SQ  SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

Query Match 43.6%; Score 869.5; DB 13; Length 347;
Best Local Similarity 54.3%; Pred. No. 3.4e-54;
Matches 165; Conservative 54; Mismatches 84; Indels 1; Gaps 1;

QY 74 CPGCCQCYRVVHCSDGLGTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 40 CPGCCQCYRVVHCSDGLGTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 99

QY 134 NNLTKIHPKAFITTKKLRRLYLHNSQLSEIPLNLPKSLABELRIHENVKVKIKQDTFKGM 193
DB 100 NNLTKIHPKAFAPMVSLDKLYISHNRLTEVPTGPPSLIELRVHENLTKRVPKDTFINN 159

QY 194 NALHVLMSANPLDNNIGIEGAFEGV-TVFHRTAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 160 GQHVHTEIGKNPSSGIEVGAFAFGNLDKLTYSKLTQPKLPNSLLEHLEGNEI 219

QY 253 STVELEDFKRYKELQRLGIGNNKITDIENGLANIPRVREIHLNENKIKKIPSGLPKLY 312
DB 220 VAIEDEDFGYPYLFRLGLSYNKTITEVQNGSLAVSGNRELHLDNNLLVSPGGLSKLRS 279

313 LQITFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNPNVYKWEQPAITFCVLSRMSV 372
DB 280 LNVVYLHNSNKEIVKPTDFCPTVSPKRAQYAGISLYDNPVKYWEVPPSVFRCVHNHNAI 339

QY 373 QLGN 376
DB 340 HFGS 343

RESULT 7
Q9DD29 ID Q9DD29 PRELIMINARY; PRT; 388 AA.
AC Q9DD29;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Biqlycan-like protein 1 (Fragment).
GN BGL1.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biqlycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247826; AAG40161.1; -.
ZFIN; ZDB-GENE-010102-1; dcn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 4.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 7.
FT NON_TER 1
FT SEQUENCE 388 AA; 42542 MW; 2E07169E9B6071B CRC64;

Query Match 43.4%; Score 865.5; DB 13; Length 388;
Best Local Similarity 54.3%; Pred. No. 7.5e-54;
Matches 165; Conservative 53; Mismatches 85; Indels 1; Gaps 1;

QY 74 CPGCCQCYRVVHCSDGLGTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 81 CPGCCQCYRVVHCSDGLGTSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 140

QY 134 NNLTKIHPKAFITTKKLRRLYLHNSQLSEIPLNLPKSLABELRIHENVKVKIKQDTFKGM 193

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DB 141 NNLTKIHPKAFAPMVSLDKLYISHNRLTEVPTGPPSLIELRVHENLTKRVPKDTFINN 200
QY 194 NALHVLMSANPLDNNIGIEGAFEGV-TVFHRTAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 201 GRUHVIELGKNPSSGIEVGAFAFGNLDKLTYSKLTQPKLPNSLLEHLEGNEI 260
QY 253 STVELEDFKRYKELQRLGIGNNKITDIENGLANIPRVREIHLNENKIKKIPSGLPKLY 312
DB 261 VAIEDEDFGYPYLFRLGLSYNKTITEVQNGSLAVSGNRELHLDNNLLVSPGGLSKLRS 320
QY 313 LQITFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNPNVYKWEQPAITFCVLSRMSV 372
DB 321 LNVVYLHNSNKEIVKPTDFCPTVSPKRAQYAGISLYDNPVKYWEVPPSVFRCVHNHNAI 380
QY 373 QLGN 376
DB 381 HFGS 384

RESULT 8
Q9DE01 ID Q9DE01 PRELIMINARY; PRT; 224 AA.
AC Q9DE01;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Decorin (Fragment).
GN DCN.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biqlycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247824; AAG40159.1; -.
ZFIN; ZDB-GENE-010102-1; dcn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 7.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00369; LRR_Typ; 7.
FT NON_TER 1
FT NON_TER 224
FT SEQUENCE 224 AA; 24442 MW; 54A1B7AB91667DF0 CRC64;

Query Match 32.1%; Score 638.5; DB 13; Length 224;
Best Local Similarity 56.5%; Pred. No. 5.6e-38;
Matches 126; Conservative 37; Mismatches 59; Indels 1; Gaps 1;

QY 94 SVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILNENKIKKIPKAFITTKLRR 153
DB 2 TVPEKIPDLDTTLLDLQNNKIKEIKENDFKGLTSLYGLILNENKIKKIPKAFITTKLRR 61

QY 154 LYLHNSQLSEIPLNLPKSLABELRIHENVKVKIKQDTFKGMNALHVLMSANPLDNNIGIEP 213
DB 62 LYLHNSQLSEIPLNLPKSLABELRIHENVKVKIKQDTFKGMNALHVLMSANPLDNNIGIEP 121

QY 214 GAFEGV-TVFHRTAEAKLTSPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLG 272
DB 122 GAFADLKRVSAIRIADTNLTSPKGLPSSLPFELHDGDKITKVTADSLKGLNLSKLS 181

QY 273 NNLTKIENGLANIPRVREIHLNENKIKKIPSGLPKLYLOI 315
DB 182 HNEISVWENGSLANVPHIRELHLENNALTAVPAGLADHKYIOV 224

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RESULT 9					
ID	Q9CTL6	PRELIMINARY;	PRT;	108 AA.	
DT	O9CTL6;				
DT	01-JUN-2001 (TrEMBLrel. 17, Created)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	463140IG09Brik protein (Fragment).				
GN	ASP_N OR 463140IG09RIK.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
STRAIN=C57BL/6J; TISSUE=EYEBALL;					
MEDLINE=21085660; PubMed=11217851;					
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,					
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,					
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,					
Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saio R.,					
Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,					
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,					
Kuehl P., Lewis S., Masters L., Nakai I., Pesole G., Quackenbush J.,					
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,					
Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,					
Blake J., Boffelli D., Bojunda N., Carninci R., de Bonaldo M.F.,					
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,					
Gustincich S., Hill D., Hofmayer C., Hume D.A., Kamiya M., Lee N.H.,					
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,					
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,					
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,					
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,					
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,					
Hayashizaki Y.;					
RT ! "Functional annotation of a full-length mouse cDNA collection";					
Nature 409:685-690(2001).					
RL Nature 409:685-690(2001).					
DR EMBL; AK021386; BAB32393.1; -.					
DR MGD; MGI:1913945; Aspn.					
DR InterPro; IPRO00372; LRR_Nterm.					
DR Pfam; PF01462; LRNT; 1.					
DR SMART; SM00013; LRNT; 1.					
FT NON_TER 108 108					
SEQUENCE 108 AA; 12303 MW; 0BD4358D35949FFA CRC64;					
Query Match 26.1%; Score 520; DB 11; Length 108;					
Best Local Similarity 84.2%; Pred. No. 6.3e-30;					
Matches 96; Conservative 6; Mismatches 6; Indels 6; Gaps 1;					
Qy 1 MKEYVLLFLALCSAKPFSPSHALTANMLKMEDTDDDDDDDDDEDNSLPPTRE 60					
Dd 1 MKEYVLLLVAVCSAKPFSPSHALTANMLKMEDTDDDDDDDD-----DNSLPPTKE 54					
Qy 61 PRSHFPFDLPVPCGFCQCYSRVVHSCDLGLTSVPNTIPDFTRMLDLONNKIK 114					
Dd 55 PVNPFPEDLPFTCFPGCQCYSRVVHSCDLGLTSVPNTIPDFTRMVDLONNKIK 108					
RESULT 10					
O94769	PRELIMINARY;	PRT;	699 AA.		
ID O94769					
AC O94769;					
DT 01-MAY-1999 (TrEMBLrel. 10, Created)					
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)					
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)					
DE Extracellular matrix protein.					
GN ECM2.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC018370.1; AAH18370.1; -;  
DR InterPro: IPR003961; FN.III.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Cterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003591; LRR\_typ.  
DR InterPro: IPR001211; PhospholipaseA2.  
DR Pfam: PF00041; fn3; 1.  
DR Pfam: PF00560; LRR; 7.  
DR Pfam: PF01463; LRRCT; 1.  
DR Pfam: PF01462; LRRNT; 1.  
DR PRINTS: PR00019; LEURICHRPT.  
DR SMART: SM00370; LRR; 3.  
DR SMART: SM00082; LRRCT; 1.  
DR SMART: SM00013; LRRNT; 1.  
DR SMART: SM00369; LRR\_TYP; 8.  
DR PROSITE: PS00119; PA2\_ASP; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 674 AA; 74087 MW; 38AB53F7243166CC CRC64;

Query Match 18.2%; Score 363.5; DB 4; Length 674;  
Best Local Similarity 32.7%; Pred. No. 7.8e-18;  
Matches 92; Conservative 51; Mismatches 105; Indels 33; Gaps 7;

QY 74 CPEGCQCYSRVHCSDGLGTSVPTNPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133  
DB 54 CFSVCRDNGFYICNDRLGTSIPADIPDDATLYLQNNQI-----N 94  
QY 134 NKKLTIKHPKAFITTKLRRLLYSHNQLSEIPLNPKSLAEIRHENKVKIKOIKDTFGM 193  
DB 95 NAGI----PQDLKTKVNVQVLYLNDLDEFPINLPSRLHLDQNNVRIIARDSLARI 150  
QY 194 NALHVLMSANPLDNNNGIEPGAF-EGVTVFHIRTAFAKLTSPKGLPPTLLELDYNKI 252  
DB 151 PLEKHLHDNDSVTSVTEEDAFADSKGLLFUSRNHLSSIPGLPTEELRLDNR 210  
QY 253 STVELEDFKRYKELQRLGLGNKKITD--IENGSLANIPRVREIHLNKKKKIPSGPEL 310  
DB 211 STPLHAFKGLNSRLRLVDGNLANQRIADDTFSRLQNLTELSLVRNSLAAPLNLP- 269  
QY 311 KYLQIFLHNSIARVGVNDFCPTVPKMKKSLYSALSIFNN 351  
DB 270 AHLQKLYLDNAISHIPYN---TLAKMRE--LERLDLSNN 304

RESULT 12

Q9DE02 ID Q9DE02 PRELIMINARY; PRT; 120 AA.

AC Q9DE02;  
Q9DE02;  
01-MAR-2001 (TREMBLrel. 16, Created)  
01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Biglycan-like protein 3 (Fragment).

GN BGL3 OR BGL3.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20496956; PubMed=11040287;  
RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;  
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";  
RL J. Mol. Evol. 51:363-373(2000).  
DR EMBL: AF247823; AAG40158.1; -;  
DR ZFIN: ZDB-GENE-010131-5; bgl3.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003591; LRR\_typ.  
DR Pfam: PF00560; LRR; 4.

DR SMART: SM00370; LRR; 3.  
DR SMART: SM00369; LRR\_TYP; 4.  
FT NON\_TER 1  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13569 MW; 37A302FB59F97696 CRC64;  
Query Match 17.8%; Score 354; DB 13; Length 120;  
Best Local Similarity 56.8%; Pred. No. 4.7e-18;  
Matches 67; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 95 VPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNKKLTIKHPKAFITTKKLRL 154  
DB 2 VPKDIPANTLLDLQNNQITETKEDDFKGLDNLIALFLNNOISKIHPKAFRMDKIL 61  
QY 155 YLSHNLSEIPLNPKSLAEIRHENKVKIKOIKDTFGMNAHVLMSANPLDNNGIE 212  
DB 62 HLSYNLLTQMPENLPISVQSLRLHDNKKISRLPKGAFKGMHDLNVLSEANSPIANSID 119

RESULT 13

Q9WVC1 ID Q9WVC1 PRELIMINARY; PRT; 796 AA.

AC Q9WVC1;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE SLIT-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE DAWLEY;  
RX MEDLINE=99292758; PubMed=10364234;  
RA Liang Y., Annan R.S., Carr S.A., Popp S., Mevissen M., Margolis R.K.,  
RA Margolis R.O.;  
RT "Mammalian homologues of the Drosophila slit protein are ligands of  
RT the heparan sulfate proteoglycan glypican-1 in brain.";  
RL J. Biol. Chem. 274:17885-17892(1999).  
DR EMBL: AF141386; AAD38940.2; -;  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Cterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003591; LRR\_typ.  
DR Pfam: PF00560; LRR; 13.  
DR Pfam: PF01463; LRRCT; 3.  
DR Pfam: PF01462; LRRNT; 4.  
DR PRINTS: PR00019; LEURICHRPT.  
DR SMART: SM00370; LRR; 7.  
DR SMART: SM00082; LRRCT; 3.  
DR SMART: SM00013; LRRNT; 4.  
DR SMART: SM00369; LRR\_TYP; 4.  
SQ SEQUENCE 796 AA; 89542 MW; 0F50806FC0345005 CRC64;

Query Match 17.1%; Score 340.5; DB 11; Length 796;

Best Local Similarity 26.1%; Pred. No. 4.1e-16;  
Matches 111; Conservative 55; Mismatches 120; Indels 139; Gaps 13;

QY 74 CPEGCQCYSRVHCSDGLGTSVPTNPFDTRMLDL 108  
DB 277 CPIACTCSNNIVDCRGKGLTEIPTNLP-EHTEIRLEQNSIRVIPPCCATSPYKKLRDL 335  
QY 109 QNNKIKEIKENDFKGLTSLYGLILNKKLTIKHPKAFITTKLRRLLYSHNQLSEIPLN 168  
DB 336 SNNQISELAPDAFQGLRSLNSLYGNKIKTELPSKLFEGLSQLLLNANKINCLRVDA 395  
QY 169 PKSLAEIR---IHENKVKIKOIKDTFGMNAHVLMSANP-----LDNNGIE 212  
DB 396 FQDLHNLNLLSYDNKIQTVAKGTFESALRAIQTMHLAQNPFTCDCHLKWLDLYLHTNPIE 455  
QY 213 -PGA-----FEGVTVFH 223

Db 456 TSGARCTSPRLANKRIGQIKKKFKRSGPTEYRSKLSGDCFADLACPEKRCCEGTV-- 513  
QY 224 IRTAEAKLTSPKGLPPTLELHLDYNKISTVELED-FKRYKELQRLGLGNKNTDIENG 282  
Db 514 -DCSNQKLNKIPHIPOYTAEELRNNEFTVLEATGIFKLPQRLKINLSNKKITDIEG 572  
QY 283 SLANIPRVREIHNENKLLK----KIPSGPELKYQIIFLHNSIARVGVNDFCPTVPKM 338  
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFGLSLAKTL---MLRSNRISCVGNDSFTGLGSVR 629  
QY 339 KKSLEY-----SATSFLNPNVKKYEMOPATERC-----VLSRMS 371  
Db 630 LLSLYDNQITTVAPGAFGLTSLSLTNLLANP-----PNCNCHLAWLGEWLRKR 679  
QY 372 VOLGN 376  
680 IVTGN 684

Query Match 16.9%; Score 336; DB 4; Length 1525;  
Best Local Similarity 26.5%; Pred. No. 1.9e-15;  
Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps 12;

QY 74 CPFGCQCYSRVHVCSDLGLTSVPTNIPEDT-----RMLDL 108  
Db 277 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVIPGAFSPYKKLRIDL 335  
QY 109 QNNKIKETIKENDFKGLTSYGLILNNKLTIKIHPKAFITTKLRLLYLSHNSLSEIPLNL 168  
Db 336 SNNQISELAPDAFOGLRSLNSLVYGNKITELPKSLFEGFLSLOLLNANKINCLRVDA 395  
QY 169 PKSLAELR---IHENKVKIKQDKTFKGMNALHVLMSANP-----LNNNGIE 212  
Db 396 FOOLHNLNLLSLYDNKIQITIAKGTFSPLRAIQTMHLAQNPFICDCHLKWLDYLTNPTE 455  
QY 213 -PCA-----FEQGVTVFH 223  
Db 456 TSGARCTSPRLANKRIGQIKKKFKRSGTGYRSKLSGDCFADLACPEKRCCEGTV-- 513  
QY 224 IRTAEAKLTSPKGLPPTLELHLDYNKISTVELED-FKRYKELQRLGLGNKNTDIENG 282  
Db 514 -DCSNQKLNKIPHIPOYTAEELRNNEFTVLEATGIFKLPQRLKINFSNKKITDIEG 572  
QY 283 SLANIPRVREIHNENKLLK----KIPSGPELKYQIIFLHNSIARVGVNDFCPTVPKM 338  
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFGLSLAKTL---MLRSNRITCVGNDSF-----I 623  
QY 339 KKSLEYSAISLENNPKYKWEQATFRCVLSRMSVOL 374  
Db 624 GLSSVLLSLYDNQIT--TVAPGAFDTLSLSTLNL 657

RESULT 15  
094813  
ID 094813 PRELIMINARY; PRT; 1529 AA.  
AC 094813;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE SLIT-2 protein.  
GN SLIT-2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99033071; PubMed=9813312;  
RA Itoh A., Miyabayashi T., Ohno M., Sakano S.;  
RT "Cloning and expressions of three mammalian homologues of drosophila  
RT slit suggest possible roles for slit in the formation and maintenance  
RT of the nervous system."  
RL Brain Res. Mol. Brain Res. 62:175-186(1998).  
RL EMBL; AB017168; BAA35185.1; -.  
RL HSSP; P00743; ICCF.  
DR InterPro; IPR000152; Asx\_hydroxyl.

Db 456 TSGARCTSPRLANKRIGQIKKKFKRSGPTEYRSKLSGDCFADLACPEKRCCEGTV-- 513  
QY 224 IRTAEAKLTSPKGLPPTLELHLDYNKISTVELED-FKRYKELQRLGLGNKNTDIENG 282  
Db 514 -DCSNQKLNKIPHIPOYTAEELRNNEFTVLEATGIFKLPQRLKINLSNKKITDIEG 572  
QY 283 SLANIPRVREIHNENKLLK----KIPSGPELKYQIIFLHNSIARVGVNDFCPTVPKM 338  
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFGLSLAKTL---MLRSNRISCVGNDSFTGLGSVR 629  
QY 339 KKSLEY-----SATSFLNPNVKKYEMOPATERC-----VLSRMS 371  
Db 630 LLSLYDNQITTVAPGAFGLTSLSLTNLLANP-----PNCNCHLAWLGEWLRKR 679  
QY 372 VOLGN 376  
680 IVTGN 684

Query Match 16.9%; Score 336; DB 4; Length 1525;  
Best Local Similarity 26.5%; Pred. No. 1.9e-15;  
Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps 12;

QY 74 CPFGCQCYSRVHVCSDLGLTSVPTNIPEDT-----RMLDL 108  
Db 277 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVIPGAFSPYKKLRIDL 335  
QY 109 QNNKIKETIKENDFKGLTSYGLILNNKLTIKIHPKAFITTKLRLLYLSHNSLSEIPLNL 168  
Db 336 SNNQISELAPDAFOGLRSLNSLVYGNKITELPKSLFEGFLSLOLLNANKINCLRVDA 395  
QY 169 PKSLAELR---IHENKVKIKQDKTFKGMNALHVLMSANP-----LNNNGIE 212  
Db 396 FOOLHNLNLLSLYDNKIQITIAKGTFSPLRAIQTMHLAQNPFICDCHLKWLDYLTNPTE 455  
QY 213 -PCA-----FEQGVTVFH 223  
Db 456 TSGARCTSPRLANKRIGQIKKKFKRSGTGYRSKLSGDCFADLACPEKRCCEGTV-- 513  
QY 224 IRTAEAKLTSPKGLPPTLELHLDYNKISTVELED-FKRYKELQRLGLGNKNTDIENG 282  
Db 514 -DCSNQKLNKIPHIPOYTAEELRNNEFTVLEATGIFKLPQRLKINFSNKKITDIEG 572  
QY 283 SLANIPRVREIHNENKLLK----KIPSGPELKYQIIFLHNSIARVGVNDFCPTVPKM 338  
Db 573 AFEAGSGVNEILLTSNRLENVQHKMFGLSLAKTL---MLRSNRITCVGNDSF-----I 623  
QY 339 KKSLEYSAISLENNPKYKWEQATFRCVLSRMSVOL 374  
Db 624 GLSSVLLSLYDNQIT--TVAPGAFDTLSLSTLNL 657

RESULT 15  
094813  
ID 094813 PRELIMINARY; PRT; 1529 AA.  
AC 094813;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE SLIT-2 protein.  
GN SLIT-2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99033071; PubMed=9813312;  
RA Itoh A., Miyabayashi T., Ohno M., Sakano S.;  
RT "Cloning and expressions of three mammalian homologues of drosophila  
RT slit suggest possible roles for slit in the formation and maintenance  
RT of the nervous system."  
RL Brain Res. Mol. Brain Res. 62:175-186(1998).  
RL EMBL; AB017168; BAA35185.1; -.  
RL HSSP; P00743; ICCF.  
DR InterPro; IPR000152; Asx\_hydroxyl.

```
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003645; FcIn.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FcIn; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 6.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1529 AA; 109869 MW; 5D19CC5E7FD461BA CRC64;

Query Match 16.9%; Score 336; DB 4; Length 1529;
Best Local Similarity 26.08; Pred. No. 1.9e-15;
Matches 105; Conservative 61; Mismatches 120; Indels 118; Gaps 12;

QY 74 CPFGQCYSRVVHCSDGLTSVPTNIPDPT-----RMLDL 108
DB 273 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVPPGAFSPYKKLRIDL 331

QY 109 ONNKIKETKENDFKLTSYGLILNNKLTIKHPKAEITTKLRRLYLSHNOISEIPNL 168
DB 332 SNNQISELPADAFQGLRSLNLYGNKTELPSLEGLFSQLQLLLNANKINCLRVA 391

QY 169 PKSLAELR---IHENKVKIKQDTFGMNAHLVLEMSANP-----LDNNGIE 212
DB 392 FQDLHNLNLSLYDNKLOTIAKTFSPRAIQTMHLAQNPFICDCHLKLWADYLHTNP 451

QY 213 -----PGA----- 215
DB 452 TSGARCTSPRLANKRIGQIKSKKFCRSKAEQYFIPGTEDYRSKLSGDCFADLACPEKCR 511

QY 216 FEGVTVEHRIAEAKLTSPKGLPPTLLEHLHDYKNKISTVELED-FKRYKELQFLGLGNN 274
DB 512 CEGTIV---DCSNOKLNKIPHIPOYTAEURLNNEFTVLEATGIFKKLPOLRKINFSNN 568

QY 275 KITDIENGLANIPRVREIHLNENKLNK-----KIPSGLPKELKYLQIIEHNSIARVGND 330
DB 569 KITDIEGAFEGASGVNEILTSNRLENVQHKMKFGLESKLT---MLRSNRITCVGND 625

QY 331 FCPVTPKMKSLYSALFNPNPKYWEQPAATFCVLIRMSVOL 374
DB 626 F-----ICLSSVRLSLYDNOIT--TVAPGAFDTLHSLSTLNL 661
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Search completed: May 27, 2003, 16:05:11  
Job time : 39 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2003, 16:01:11 ; Search time 22 seconds  
(without alignments)  
1656.134 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFFS.....PATERCVLSRMSVOLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR73:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1040.5	52.2	369	2 S32793	biglycan precursor
2	1037.5	52.1	369	2 S20811	proteoglycan I - m
3	1034	51.9	368	1 BGHUN	biglycan precursor
4	1024.5	51.4	369	2 S32559	biglycan precursor
5	969	48.6	357	2 S24317	decorin precursor
6	963.5	48.4	359	1 NBHUC8	decorin precursor
7	943	47.3	360	2 S06280	decorin precursor
8	941	47.2	360	2 I47020	decorin - rabbit
9	907.5	45.6	354	2 A35454	decorin precursor
10	899	45.1	354	2 S29145	decorin precursor
11	399.5	20.1	343	2 A41748	lumican precursor
12	384	19.3	342	2 A46743	lumican precursor
13	378	19.0	338	2 S52284	lumican precursor
14	358.5	18.0	382	2 I39088	lumicon, secretory
15	342.5	17.2	375	2 S05390	proline-arginine-
16	333.5	16.7	380	2 S71876	fibromodulin precu
17	324	16.3	1523	2 T13953	fibromodulin - chi
18	323	16.2	1531	2 T42218	MEGF5 protein - ra
19	318	16.0	376	2 S52275	slit-1 protein hom
20	316	15.9	1469	2 B36665	fibromodulin precu
21	296	14.9	1091	2 A36665	slit protein 2 pre
22	294	14.8	361	2 A58532	slit protein 1 pre
23	282.5	14.2	1025	2 A53860	glial cell membran
24	272	13.7	603	2 J42626	chondroadherin pre
25	266	13.4	707	2 JC1282	secreted leucine-r
26	265	13.3	603	2 JC7763	insulin-like growt
27	265	13.3	603	2 JC6128	neuronal leucine-r
28	261.5	13.1	907	2 T13174	insulin-like growt
29	261.5	13.1	907	2 JG0193	gp150 protein - fr
					G protein-coupled

## ALIGNMENTS

RESULT 1  
S32793

biglycan precursor - rat

N:Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteoglycan I core prot  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change 20-Aug-1999  
C:Accession: S32793

R:Dröher, K.L.; Asundi, V.; Matzura, D.; Cowan, K.

Eur. J. Cell Biol. 53, 296-304, 1990

A:Title: Vascular smooth muscle biglycan represents a highly conserved proteoglycan w  
A:Reference number: S32793; MUID:91184222; PMID:2081545

A:Accession: S32793

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-369 <DRE>

A:Cross-references: GB:U17834; NID:g600497; PIDN:AA58797.1; PID:g600498

C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc  
C:Keywords: Chondroitin sulfate proteoglycan; dermatan sulfate; extracellular matrix;  
F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-37/Domain: propeptide #status predicted <PRO>

F:38-369/Product: biglycan #status predicted <PRO>

F:58-82/Domain: proteoglycan amino-terminal homology <PAH>

F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F:255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F:279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F:302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical

F:317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>

F:42,48,181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted

F:271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 52.2%; Score 1040.5; DB 2; Length 369;

Mismatches 199; Conservative 67; Mismatches 93; Indels 19; Gaps 3;

Qy 4 YVLLFLALCSAKPF----FSPSHIALKNMLKMDTDDDDDDDDDDDDNSLPFTR 59

Db 5 WLLTLLALSCALPFEQKGFWDFTLDGLLMDNEEASGSDTTSGVPDL- ---SLTPT- 59

Qy 60 EPRSHFFPDLFPMCPGCGOCYRVVHCSDLGTSVPTNTPTFTRMLDQNNKIKETKEN 119

Db 60 -----FSAMCPGCHCLRVVQCSDLGKTVPKETSPDTLLDQNNISELRKD 109

Qy 120 DFKGLTSLYGLILNNKLTTHPKAFLTTKRLRLYSHNQLSEIPLNLPKPSLAELRIHE 179

Db 110 DFKGLQHLVYLVNKKISKIHEKAFSPRLKQKLYISKNNHLVEIPNLPSSSLVELRIHD 169

4 YVLLFLALCSAKPP- ---FSPSHIALKNMMLKQMEDTDDDDDDDDDDDDDDSDNSLSFPTTR 59  
 5 WLLTLLALLSQAFLPEQKGFWDFTLDDGLLMMNDDEASGSDTTSVGPDL- ---SVTPT- 59  
 60 EPRSHFFPDLFPMGPGQCQCYSRVHVSGLTSTVPTNIPDTRMLDLQNNKIKIEN 119  
 60 - - - - -FSAMCPFGCHLRVWQCSDGLKTVKPEISPDTTLLDLQNNDI1SELKRD 109  
 120 DFKGLTSLYGLLNNKLTTHPKAFLTTKKLRRLYLSHNQSLSEPLNLPKSLAEFLRTH 179  
 110 DFKGLQHLVYALVNVNKKTSIKHEKAFSPURKLOKLYISKNLHVEIPLNLPSSLEVERLHD 169  
 180 NKVKTKQKDTKGMNALHWLENSANPLDNNNGTEPGAEGVTVFHIRIAEAKLTSPVKGLP 239  
 170 NRIRKVPKGVSSCLRNMCNMIEMGNPNLENSGEPGAFDGLKLNLYLRISAKLTGIPKDL 229  
 240 PTLLELHLDYNNISTVLEDFEYKRELOBLGLGNKNTIDTENGSLANIPRVREIHLNNK 299  
 230 ETNLNHLHNNKIQATELDLRLYSKLYRLGLGHQNIQIRMIENGSLSFLETLRELHLNNK 289  
 300 LKKIPSLPELXYLQILFIHLSNSTARGVNDRCPTVPKMKKSLYSALSFNNPNPVYWENO 359  
 290 LSRVPAGLPLDLQVYVHLSNNITKVGINDFCPMGFGVKRAYNGISLFNNPNPVYWEVQ 349  
 360 PATFRCVLSRMSVOLGNF 377  
 350 PATFRCVTDLAIQFGNY 367  
 RESULT 3  
 BGHUN  
 N:Alternate names: cartilage proteoglycan I; dermatan sulfate proteoglycan I (DS-PGI)  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Apr-1992 #sequence\_revision 26-May-1995 #text\_change 28-Jan-2000  
 C:Accession: A40757; I38706; A32458; S14349; S05639; A28457  
 R:Fisher, L.W.; Heegaard, A.M.; Vetter, U.; Vogel, W.; Just, W.; Termine, J.D.; Young  
 J. Biol. Chem. 266, 14371-14377, 1991  
 A:Title: Human biglycan gene. Putative promoter, intron-exon junctions, and chromoso  
 A:Reference number: A40757; MUID:91317791; PMID:1860845  
 A:Accession: A40757  
 A:Molecule type: DNA  
 A:Residues: 1-368 <FIS1>  
 A:Cross-references: GB:M65151; NID:gl79428; GB:M65152; NID:gl79429; GB:M65153; NID:gl  
 A:Note: the translated sequence in GenBank entry HUMBGN3, release 113.0, (PIDN:AAA522  
 d not the DNA) and 26 residues inserted after residue 80 (apparently from a misread s  
 R:Just, W.; Rau, W.; Muller, R.; Geerikens, C.; Vogel, W.  
 Hum. Mol. Genet. 3, 2268, 1994  
 A:Title: Dinucleotide repeat polymorphism at the human biglycan (BGN) locus.  
 A:Reference number: I38706; MUID:95187185; PMID:7881444  
 A:Accession: I38706  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 361-368 <JUS>  
 A:Cross-references: EMBL:U11686; NID:g607862; PIDN:AAC50117.1; PID:g619663  
 R:Fisher, L.W.; Termine, J.D.; Young, M.F.  
 J. Biol. Chem. 264, 4571-4576, 1989  
 A:Title: Deduced protein sequence of bone small proteoglycan I (Biglycan) shows homol  
 A:Reference number: A32458; MUID:89174714; PMID:2647739  
 A:Accession: A32458  
 A:Molecule type: mRNA  
 A:Residues: 1-138, 'NV', 141-162, 'DV', 165-368 <FIS2>  
 A:Cross-references: GB:J04599; NID:g184339  
 A:Note: parts of this sequence, including the amino end of the mature protein, were d  
 A:Note: the translated sequence in GenBank entry HUMHPG1, release 113.0, (PIDN:AAA360  
 R:Stoecker, G.; Meyer, H.E.; Wagener, C.; Greiling, H.  
 Biochem. J. 274, 415-420, 1991  
 A:Title: Purification and N-terminal amino acid sequence of a chondroitin sulphate/de  
 A:Reference number: S14349; MUID:91174749; PMID:1848758  
 A:Accession: S14349  
 A:Molecule type: protein  
 A:Residues: 38-57 <STO>  
 A:Experimental source: aorta

R:Roughley, P.J.; White, R.J.  
 Biochem. J. 262, 823-827, 1989  
 A:Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties of  
 A:Reference number: S05639; MUID:90073579; PMID:2590169  
 A:Accession: S05639  
 A:Molecule type: protein  
 A:Residues: 38-41, 'X', 43-46, 'X', 48-57 <ROU>  
 R:Fisher, L.W.; Hawkins, G.R.; Tuross, N.; Termino, J.D.  
 J. Biol. Chem. 262, 9702-9708, 1987  
 A:Title: Purification and partial characterization of small proteoglycans I and II, bone  
 A:Reference number: A92656; MUID:87250639; PMID:3597437  
 A:Accession: A28457  
 A:Molecule type: protein  
 A:Residues: 38-41, 'X', 43-62, 'X', 64-66 <FIS3>  
 A:Experimental source: bone  
 C:Genetics:  
 A:Gene: GDB:BGN  
 A:Cross-references: GDB:119727; OMIM:301870  
 Map position: Xq28-Xq28  
 A:Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3  
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
 C:Keywords: chondroitin sulfate proteoglycan; dermatan sulfate; duplication; extracellular  
 F:1-16/Domain: signal sequence #status predicted <SIG>  
 F:17-37/Domain: propeptide #status predicted <PRO>  
 F:38-368/Product: biglycan #status predicted <MAT>  
 F:57-81/Domain: proteoglycan amino-terminal homology <PAH>  
 F:91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:115-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:139-159/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:160-183/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:184-207/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:209-229/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F:230-253/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F:254-277/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F:278-300/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:301-315/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
 F:316-368/Domain: proteoglycan carboxyl-terminal homology <PCH>  
 F:42, 47/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
 F:180, 198/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
 F:270, 311/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 1034; DB 1; Length 368;  
 Best Local Similarity 53.2%; Pred. No. 3 4e-63;  
 Matches 200; Conservative 63; Mismatches 93; Indels 20; Gaps 3;

6 LLEFLAICSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFTREP 61  
 7 LVSLALSQLPFEQRFQDFDFTLDDGPFMMNDREASGADTSGVLPD-----SVIPTY- 60  
 QY 62 RSHFFPDLFPMCPFCOCYSRVVHCSDGLTSVPTNIFDTRMLDLQNNKKEIKENDF 121  
 Db 61 -----AMCPFGCHLRVVOCSDLGLSVKPEISPDPTLLDLQNNDISLRKDDF 110  
 QY 122 KGTLGYLGLNNKTKIHPKAFITTKLRRLYLSHNOLSEIPLNPKSLAEIRTHENK 181  
 Db 111 KGQLHYALVLYNNKISKIHERAFSLRKLQKLYTSKNHVEIPNPLPSVLRIHDNR 170  
 QY 182 VKIQDPTFGMMALHVLMSANPLDNNIGEPAGFVGTVFHIRIAEAKLTSVPKGLPPT 241  
 Db 171 IRKVPKGVFSGLNMMNCIEMGGNPLNSGFEFGADGLKLVLRISAKLTGPKDLPPT 230  
 QY 242 LLEHLYNNKISVLEDEPKRYKELQRLGLGNKTKITDIENGLANTIPRVREHLNNK 301  
 Db 231 LNEHLHNNKIQAELEDLRLYSKLYRGLGHQNRMIENGSLSPFTLRLEHLDDNNK 290  
 QY 302 KIPSGLPKLYLQIIFLHNSIARVGVNDFCPVPMKKSLSAISLFPNNPVKYMOWE 361  
 Db 291 RVPSGLPKLLQVYLYHNSNITKVGNDVFCMPGCVKRAYNGISLFPNNPVYWEV 350  
 QY 362 TPCVLSRMSVQLGNF 377  
 Db 351 TPCVTDRLAIQFGNY 366

## RESULT 4

S32559  
 biglycan precursor - bovine  
 N:Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteochondroitin core p  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 03-May-1994 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
 C:Accession: S32559; S34229; S34701; A31430; PT0078; S55673; A33137  
 R:Torok, M.A.; Evans, S.A.S.; Marcum, J.A.  
 Biochim. Biophys. Acta 1173, 81-84, 1993  
 A:Title: cDNA sequence for bovine biglycan (PGI) protein core.  
 A:Reference number: S32559; MUID:93250052; PMID:8485158  
 A:Accession: S32559  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <TOR>  
 A:Cross-references: EMBL:L07953; NID:g162746  
 A:Experimental source: aortic smooth muscle  
 R:Marcum, J.A.; Torok, M.; Evans, S.  
 submitted to the EMBL Data Library, December 1992  
 A:Reference number: S34229  
 A:Accession: S34229  
 A:Molecule type: mRNA  
 A:Residues: 1-250, 'V', 252-369 <MAR>  
 A:Cross-references: EMBL:L07953  
 R:Neame, P.J.; Choi, H.U.; Rosenberg, L.C.  
 J. Biol. Chem. 264, 8653-8661, 1989  
 A:Reference number: A33701  
 A:Accession: A33701  
 A:Molecule type: protein  
 A:Residues: 38-187, 'E', 189-367, 'Y' <NEA>  
 A:Experimental source: cartilage  
 R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.  
 J. Biol. Chem. 264, 2876-2884, 1989  
 A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII,  
 A:Reference number: A31430; MUID:89123388; PMID:2914936  
 A:Accession: A31430  
 A:Molecule type: protein  
 A:Residues: 38-41, 'X', 43-47, 'X', 49-63 <CHO>  
 A:Note: sequences from skin and cartilage were identical  
 R:Marcum, J.A.; Thompson, M.A.  
 Biochem. Biophys. Res. Commun. 175, 706-712, 1991  
 A:Title: The amino-terminal region of a proteochondroitin core protein, secreted by a  
 com human bone.  
 A:Reference number: PT0077; MUID:91207372; PMID:2018513  
 A:Accession: PT0078  
 A:Molecule type: protein  
 A:Residues: 17-24, 'F', 26-30 <MA2>  
 A:Experimental source: aortic smooth muscle  
 R:Scott, P.G.; Nakano, T.; Dodd, C.M.  
 Biochim. Biophys. Acta 1244, 121-128, 1995  
 A:Title: Small proteoglycans from different regions of the fibrocartilaginous temporo  
 A:Reference number: S55673; MUID:95284073; PMID:7766647  
 A:Accession: S55673  
 A:Molecule type: protein  
 A:Residues: 38-41, 'X', 43-47, 'X', 49-53 <SCO>  
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc  
 C:Keywords: cartilage; chondroitin sulfate proteoglycan; dermatan sulfate; extracellu  
 F:1-16/Domain: signal sequence #status predicted <SIG>  
 F:17-37/Domain: amino-terminal propeptide #status predicted <PRO>  
 F:38-369/Product: biglycan #status predicted <MAT>  
 F:92-115/Domain: proteoglycan amino-terminal homology <PAH>  
 F:116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F:255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F:279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F:302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>

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R; Roughley, P.J.; White, R.J.

C:Accession: S06280; B31430; A26545; A20935  
R:Bay, A. A.; McQuillan, C. I.; Termino, J. D.; Young, M. R.  
Biochem. J. 248, 801-805, 1987  
A:Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan I  
A:Reference number: S06280; MUID:88133946; PMID:3435485  
A:Accession: S06280  
A:Molecule type: mRNA

A:Residues: 1-360 <DAY>  
A:Cross-references: EMBL:X00712; NID:g618; PIDN:CAA68702.1; PID:g619  
A:Experimental source: bone  
R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.  
J. Biol. Chem. 264, 2876-2884, 1989  
A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII,  
A:Reference number: A31430; MUID:89123398; PMID:2914936  
A:Accession: B31430  
A:Molecule type: protein

A;Residues: 31-33, A', 35-54 <COS>  
A;Experimental source: cartilage; fetal skin  
R;Coster, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.  
J. Biol. Chem. 262, 3809-3812, 1987  
A;Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship t  
A;Reference number: A26545; MUID:87137687; PMID:3818667  
A;Accession: A26545  
A;Molecule type: protein  
A;Residues: 31-50 <COS>  
A;Experimental source: sclera  
R;Pearson, C.H.; Winterbottom, N.; Fackre, D.S.; Scott, P.G.; Carpenter, M.R.  
J. Biol. Chem. 258, 15101-15104, 1983  
A;Reference number: A20935; MUID:84087911; PMID:6654908  
A;Accession: A20935  
A;Molecule type: protein  
A;Residues: 31-54 <PEA>  
A;Experimental source: skin

R.; Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G. *Biochem. J.* 232, 277-279, 1985

A: Reference number: A44700; PMID:86103195; PMID:3936484

A, contents; amniocentesis; glycosylation  
C, Superfamily; decorin; leucine-rich alpha-2-glycoprotein repeat homolog; proteoglyc  
D, Keywords; chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; ext  
E, 15 proteins

F:1-13/Domain: signal sequence #status predicted <SIG>  
F:16-30/Domain: propeptide #status predicted <PRO>  
F:31-360/Product: decorin #status predicted <MAT>

F:49-53/Domain: proteoglycan amino-terminal homology <PAH>  
F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F;131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRP3>  
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>  
F;176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F; 202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>  
F; 223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>  
F; 247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

	leucine-rich alpha-2-glycoprotein repeat	homology	<LRR>
F:271-293/Domain:	leucine-rich alpha-2-glycoprotein repeat <td>homology</td> <td></td>	homology	
F:294-308/Domain:	leucine-rich alpha-2-glycoprotein repeat <td>homology</td> <td></td>	homology	
F:309-350/Domain:	proteolysin carboxyl-terminal homology	homology	#status atypical

F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
F:190,326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F:212,262,204,613,326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted

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r, r12, r23, r34/Binding site: carbonylrate (Asn) (covalent) #status predicted
Query Match 47.3%; Score 943; DB 2; Length 360;
Best Match 47.3%; Score 943; DB 2; Length 360;

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best Local Similarity 49.1%; Pred. No. 5,34e-57;  
Matches 186; Conservative 69; Mismatches 102; Indels 22; Gaps 5;

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1  MKATIIFLLVAQVSWAGPF---QOKGLFDFML-----EDASGICPEEHFPFVPEI 48

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QY 60 EPRSHFFFDLFPMCPFGCQCSRVVHCSDGLT SVPTNIPFDTRMLDLONNKIKETKEN 119

Db 49 EP-----MGPPVCFRCQCHLRVQCSDGLEKVPKDPDPTALLDLQNKKITEKDG 100

QV 120 DFKGLTSLYGLIILNNKKLTIIHPKAFITTKKIRRIYISNQISPIPIINPKSIAFPIHF 79

### 6.1. FITTING ERROR WHEN A FEW DATA POINTS ARE MISSING

[illegible]

RESULT 8  
ID: 147020  
Species: rabbit  
Accession: I47020  
Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues.  
Date: 04-Sep-1997  
Revision: 04-Sep-1997  
Accession: I47020  
Author: R. Zhan, Q.; Burrows, R.; Cintron, C.  
Invest. Ophthalmol. Vis. Sci. 36, 206-215, 1995  
A: Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues.  
A: Reference number: I47020  
A: MUID: 95122319  
A: PMID: 7822148  
A: Accession: I47020  
A: Status: preliminary  
A: Translated from GB/EMBL/DDBJ  
A: Molecule type: mRNA  
A: Residues: 1-360  
A: Cross-references: GB:S76584; NID:g913374; PIDN:AAB33083.1; PID:g913375  
A: Superfamily: decorin  
A: Proteoglycan amino-terminal homology <PAH>  
A: F:49-73/Domain: proteoglycan amino-terminal homology <PAH>  
A: F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
A: F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
A: F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
A: F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
A: F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
A: F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
A: F:223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
A: F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
A: F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
A: F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
A: F:309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>

QY 299 KUKKTPSGLPELKYLYQITLPHNSSTARCVNDFCTVPKMKKSLYSALSLENNPKYIWEW 358  
 || |||||:||||:||||: || ||||| ||||| |||||:||||:||||:  
 Db 281 KLIRVGGGLADHKYIQVWYLDHNNITSVVGANDFCPPGYNTKKASYSGVSLFSNPVQYWEI 340  
 QY 359 QPATPRCVLSRMSVQLGNF 377  
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 Db 341 QPSTFRCVYMRSAIQLGNY 359  
 ||:||||| |||||:  
 RESULT 9  
 A55454  
 decarin precursor - mouse  
 N:Alternate names: proteoglycan II  
 C:Species: Mus musculus (house mouse)  
 C:Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 20-Aug-1999  
 C:Accession: A55454; S20812  
 R:Schoelzen, T.; Sollars, M.; Suzuki, S.; Suzuki, J.L.; Buchberg, A.M.; Si  
 J. Biol. Chem. 269, 28270-28281, 1994  
 A:A:Title: The murine decarin. Complete cDNA cloning, genomic organization, chromosomal  
 A:A:Reference number: A55454; M0ID:95050610; PMID:7961765  
 A:Accession: A55454  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <SCH>  
 A:A:Cross-references: GB:X53929; NID:g53668; PIDN:CAA37876.1; PID:g53669  
 R:Naitoh, Y.; Suzuki, S.  
 submitted to the EMBL Data Library, July 1990  
 A:A:Description: Nucleotide sequences of cDNAs encoding mouse PGI and PGII.  
 A:A:Reference number: S20811  
 A:Accession: S20812  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <NML>  
 A:A:Cross-references: EMBL:X53929; NID:g53668; PIDN:CAA37876.1; PID:g53669  
 C:Superfamily: decarin; leucine-rich alpha-2-glycoprotein repeat homology; proteogly  
 C:Keywords: collagen binding; extracellular matrix; glycoprotein  
 F:1-16/Domain: signal sequence #status predicted <SIG>  
 F:17-30/Domain: propeptide #status predicted <PRO>  
 F:43-67/Domain: proteoglycan amino-terminal homology <PAH>  
 F:77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F:217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F:241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F:265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical  
 F:303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>

Db 267 RELHLDNNKLLRPAGLAQHKKYIQVYVLLHNNNTISAVQNDFCRAGHPSPRKASYSAVSLYG 326

Qy 351 NPVKYWEQMPATFCVLSRMSVOLGNF 377  
||:||||:| ||||| | :||||:

Db 327 NPVRYWEIFNTFCVYVRSALQIGNY 353

RESULT 10

S29145  
decorin precursor - rat  
N:Alternate names: dermatan sulfate proteoglycan-II  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S29145; I60238; S28517  
R:Abramson, S.R.; Woessner Jr., J.F.  
Biochim. Biophys. Acta 1132, 225-227, 1992  
A:Title: cDNA sequence for rat dermatan sulfate proteoglycan-II (decorin).  
A:Reference number: S29145; MUID:93003331; PMID:1390895  
A:Accession: S29145  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-354 <ABR>  
A:Cross-references: EMBL:212298; NID:g57549; PIDN:CAA78170.1; PID:g57550  
R:Asundi, V.K.; Dreher, K.L.  
Eur. J. Cell Biol. 59, 314-321, 1992  
A:Title: Molecular characterization of vascular smooth muscle decorin: deduced core protein  
A:Reference number: I60238; MUID:93154359; PMID:1493796  
A:Accession: I60238  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 11-354 <RES>  
A:Cross-references: EMBL:X59859; NID:g56056; PIDN:CAA42519.1; PID:g56057  
C:Gene: DCN  
A:Gene: DCN  
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
C:Keywords: collagen binding; extracellular matrix; glycoprotein  
F:1-30/Domain: signal sequence (fragment) #status predicted <SIG>  
F:31-354/Product: decorin #status predicted <MAT>  
F:43-67/Domain: proteoglycan amino-terminal homology <PAH>  
F:77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F:265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F:288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR>  
F:303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 45.1%; Score 899; DB 2; Length 354;  
Best Local Similarity 46.5%; Pred No. 5.2e-54;  
Matches 178; Conservative 70; Mismatches 99; Indels 36; Gaps 5;

Qy 1 MKEYVLLFLALCS-AKPPFSPSHIALKNMKDMEDTDDDDDDDDDDDDNSLFTTR 59  
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Db 1 MKATLVFLLAQVSWAGPF---EQRGLEDFMLED----- 31

Qy 60 EPRSHPFPD----LFPNCPFGCQYSRVWHCSDLGLTSVPTNIPDFTRMLDLQNNKKE 115  
||:||||:| ||||| | :||||:

Db 32 -EASGIIPYDPNPDLISMCPYRCQCHLRVYVQSDGLGDKVPWFEPDPTLLDLQNNKITE 90  
||:||||:| ||||| | :||||:

Qy 116 IKENDPKGLTSLYGLLNNKLLTKHPKAFLTTKKLRRLYLSHNSQLSEIPLNPKSLAEL 175  
||:||||:| ||||| | :||||:

Db 91 IKEGAFKNLKDHLTLILVNNKISKISPEAFKPLVKLRLYLSKNHLKELPEKLPKTLQEL 150  
||:||||:| ||||| | :||||:

Qy 176 RIHENKVKKIQRDTFGMMNALHVENSANPLDNNNGIEPGAFEGVT-VFHIRIAEAKLTSW 234  
||:||||:| ||||| | :||||:

Db 151 RLHDNEITLKKSVFNLRMIVIELGGPNLKSNGIENGALQMGKGLGYIRSDTNITAI 210  
||:||||:| ||||| | :||||:

Qy 235 PKGLPPTLLEHLHDYNNKISTVELEDFPKRYKELQRLGLGNKKTIDTENGSLANIPRYRETH 294  
||:||||:| ||||| | :||||:

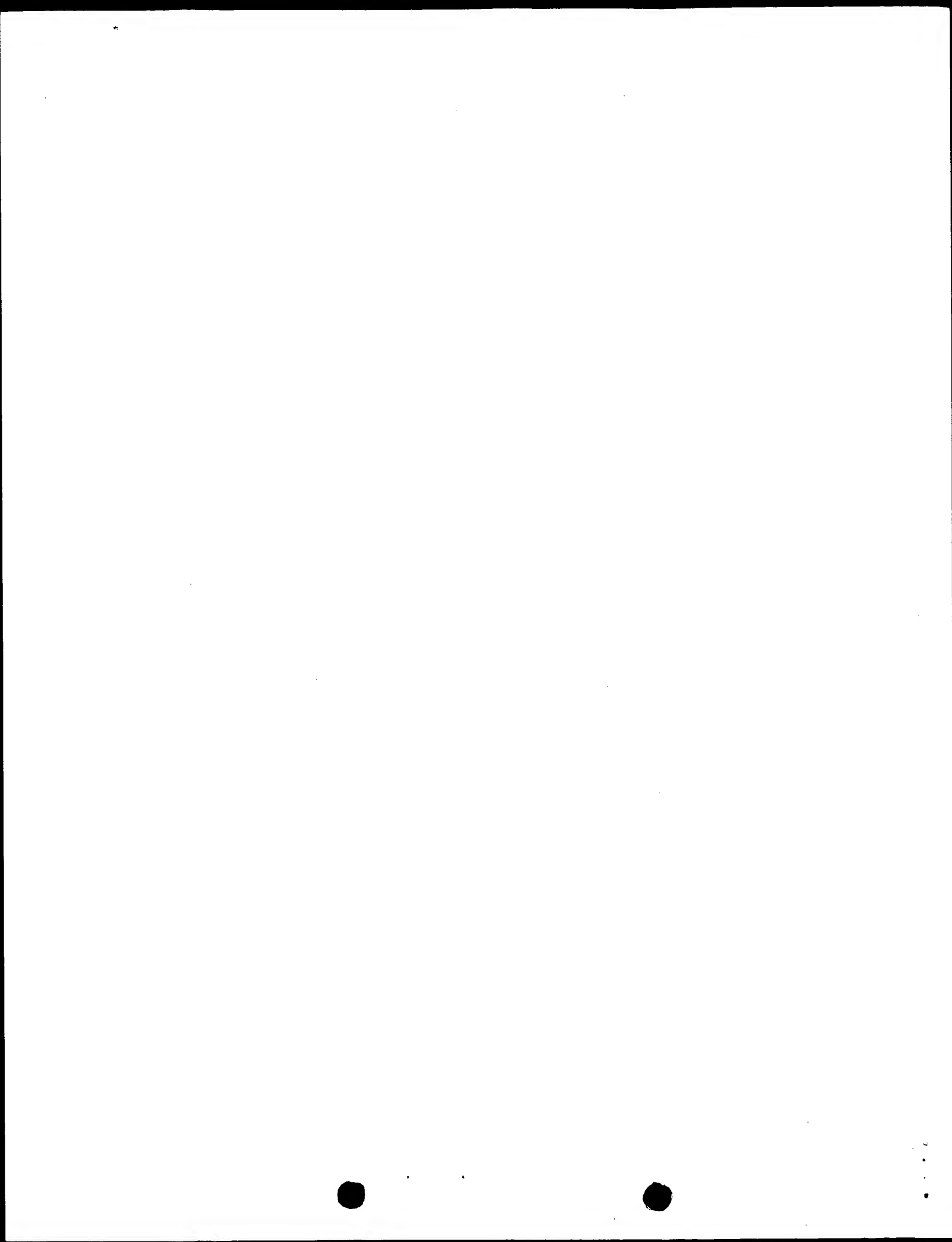






Search completed: May 27, 2003, 16:05:37  
Job time : 24 secs

Search completed: May 27, 2003, 16:05:37  
Job time : 24 secs



GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: May 27, 2003, 15:55:26 ; Search time 14 Seconds  
(without alignments)  
1122.823 Million cell updates/sec

Title: US-09-944-457-2  
Perfect score: 1992  
Sequence: 1 MKEYVLLLLFLALCSAKPFTS.....PATFRCVLSRMSVQLNFCGM 379

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1992	100.0	379	1 ASPN_HUMAN	Q9bxn1 homo sapien
2	1799	90.3	373	1 ASPN_MOUSE	Q9bmq4 mus musculus
3	1044	52.4	368	1 PGS1_XENLA	Q9lb75 xenopus lae
4	1040.5	52.2	369	1 PGS1_RAT	P47853 rattus norv
5	1037.5	52.1	369	1 PGS1_MOUSE	P28653 mus musculus
6	1034	51.9	368	1 PGS1_HUMAN	P21810 homo sapien
7	1028.5	51.6	372	1 PGS1_HORSE	O46403 equus cabal
8	1027.5	51.6	369	1 PGS1_SHEEP	O46390 ovnis aries
9	1021.5	51.3	369	1 PGS1_CANFA	O02678 canis famil
10	1019.5	51.2	369	1 PGS1_BOVIN	P21809 bos taurus
11	974	48.9	356	1 PGS2_COTJA	Q9de68 coturnix co
12	969	48.6	357	1 PGS2_CHICK	P28675 gallus gall
13	967	48.5	360	1 PGS2_PIG	Q9xsd9 sus scrofa
14	963.5	48.4	359	1 PGS2_HUMAN	P07585 homo sapien
15	947	47.5	360	1 PGS2_SHEEP	Q9tte2 ovnis aries
16	943	47.3	360	1 PGS2_BOVIN	P21793 bos taurus
17	941	47.2	360	1 PGS2_RABIT	Q28688 eryctolagus
18	939	47.1	360	1 PGS2_HORSE	O46542 equus cabal
19	934	46.9	360	1 PGS2_CANFA	Q29393 canis famil
20	907.5	45.6	354	1 PGS2_MOUSE	P28654 mus musculus
21	899	45.1	354	1 PGS2_RAT	Q01129 rattus norv
22	641	32.2	272	1 PGS1_PIG	Q9gkq6 sus scrofa
23	442	22.2	135	1 PGS1_RABIT	O46377 eryctolagus
24	399.5	20.1	343	1 LUM_CHICK	P51890 gallus gall
25	398.5	20.0	343	1 LUM_COTJA	Q9de67 coturnix co
26	390	19.6	338	1 LUM_MOUSE	P51884 homo sapien
27	384	19.3	342	1 LUM_BOVIN	O05443 bos taurus
28	383	19.2	338	1 LUM_MOUSE	P51885 mus musculus
29	378	19.0	338	1 LUM_RAT	P51886 rattus norv
30	366	18.4	421	1 OMD_HUMAN	Q99983 homo sapien
31	363.5	18.2	646	1 FLR3_HUMAN	Q9nzu0 homo sapien
32	361.5	18.1	381	1 PRLP_BOVIN	Q9gkn8 bos taurus
33	358.5	18.0	382	1 PRLP_HUMAN	P51888 homo sapien

34	356.5	17.9	377	1 PRLP_RAT	Q9eqp5 rattus norv
35	345	17.3	351	1 KERA_MOUSE	O35367 mus musculus
36	342.5	17.2	375	1 FMOD_BOVIN	P13605 bos taurus
37	342.5	17.2	378	1 PRLP_MOUSE	O91k53 mus musculus
38	340.5	17.1	352	1 KERA_BOVIN	O62702 bos taurus
39	340.5	17.1	352	1 KERA_HUMAN	O60938 homo sapien
40	338	17.0	376	1 FMOD_RAT	P50609 rattus norv
41	338	17.0	422	1 OMD_BOVIN	O77742 bos taurus
42	333.5	16.7	380	1 FMOD_CHICK	P51887 gallus gall
43	331.5	16.6	649	1 FLR3_HUMAN	Q9nzu0 homo sapien
44	331	16.6	376	1 FMOD_MOUSE	P50608 mus musculus
45	325	16.3	353	1 KERA_CHICK	O42235 gallus gall

ALIGNMENTS

RESULT 1					
ASPN_HUMAN					
ID	ASPN_HUMAN	STANDARD;	PRT;	379 AA.	
AC	Q9BXN1: Q96LDO; Q96K79;				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Asporin precursor (Periodontal ligament associated protein-1) (PLAP-1).				
DE	1).				
GN	ASPN OR PLAP1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITE				
RP	ASN-281, MASS SPECTROMETRY, AND POLYMORPHISM OF POLY-ASP REGION.				
RC	TISSUE=Cartilage;				
RX	MEDLINE=21192276; PubMed=11152692;				
RA	Lorenzo P., Aspberg A., Oennerfjord P., Bayliss M.T., Neame P.J.,				
RA	Heinegaard D.;				
RT	"Identification and characterization of asporin. A novel member of the				
RT	leucine-rich repeat protein family closely related to decorin and				
RT	biglycan."				
RL	J. Biol. Chem. 276:12201-12211(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21472263; PubMed=11587855;				
RA	Yamada S., Murakami S., Matoba R., Ozawa Y., Yokokoji T., Nakahira Y.,				
RA	Ikezawa K., Takayama S.-I., Matsubara K., Okada H.;				
RT	"Expression profile of active genes in human periodontal ligament and				
RT	isolation of PLAP-1, a novel SLRP family gene."				
RL	Gene 275:279-286(2001).				
RN	[3]				
RP	SEQUENCE OF 1-242 FROM N.A.				
RC	TISSUE=Embryo;				
RA	Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,				
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,				
RA	Wagatsuma T., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,				
RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,				
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,				
RA	Ninomiya J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,				
RA	Ninomiya K., Iwayanagi T.;				
RT	"NED0 human cDNA sequencing project."				
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	PARTIAL SEQUENCE FROM N.A.				
RX	PubMed=11152695;				
RA	Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Eberspaecher H.,				
RA	Zhou W., de Crombrughe B., Hoeck M., Mayne R.;				
RT	"Expression pattern and gene characterization of asporin. A newly				
RT	discovered member of the leucine-rich repeat protein family."				
RL	J. Biol. Chem. 276:12212-12221(2001).				
CC	-/- SUBCELLULAR LOCATION: Extracellular matrix.				
CC	-/- TISSUE SPECIFICITY: Higher levels in osteoarthritic articular				
CC	cartilage, aorta, uterus. Moderate expression in small intestine,				



FT	REPEAT	350	373	LRR-T 8.
FT	DOMAIN	36	46	POLY-ASP.
FT	DISULFID	326	359	BY SIMILARITY.
FT	CARBOHYD	48	48	N-LINKED (BY SIMILARITY).
FT	CARBOHYD	275	275	O-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE	373 AA;	42572 MW;	A50CAC82AABCF35 CRC64;

Query Match	90.38;	Score 1799;	DB 1;	Length 373;
Best Local Similarity	90.28;	Pred. No. 2.5e-117;		
Matches 341;	Conservative	17;	Mismatches 14;	Indels 6; Gaps 1;

QY	1	MKEYVLLIFLALCSAKPEFS	SHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDNSLFPPTRE	60
DB	1 <td>MKEYVMULLLAVCSAKPEFS<th>SHTALKNMMLKDMEDTDDDDDDDDDDNSLFPPTKE</th><th>54</th></td>	MKEYVMULLLAVCSAKPEFS <th>SHTALKNMMLKDMEDTDDDDDDDDDDNSLFPPTKE</th> <th>54</th>	SHTALKNMMLKDMEDTDDDDDDDDDDNSLFPPTKE	54
QY	61	PRSHFFPDLPMCPFCGCQY <th>SRVHVCSDGLGTSVPTNIPFDT</th> <th>RMLDQNNKIKEIKEND 120</th>	SRVHVCSDGLGTSVPTNIPFDT	RMLDQNNKIKEIKEND 120
DB	55	PVNFPEFPDLPTCPFCGCQY <th>SRVHVCSDGLGTSVPTNIPFDT</th> <th>RMDVLDQNNKIKEIKEND 114</th>	SRVHVCSDGLGTSVPTNIPFDT	RMDVLDQNNKIKEIKEND 114
QY	121	FKGLTSLYGLLNNKLT <th>KIHPKAFLLTKLRRRLYLSHNSQLSEIP</th> <th>LNLPKSLAEILRIHEN 180</th>	KIHPKAFLLTKLRRRLYLSHNSQLSEIP	LNLPKSLAEILRIHEN 180
DB	115	FKGLTSLYALLNNKLT <th>KIHPKFTLLTKLRRRLYLSHNSQLSEIP</th> <th>LNLPKSLAEILRIHDN 174</th>	KIHPKFTLLTKLRRRLYLSHNSQLSEIP	LNLPKSLAEILRIHDN 174
QY	181	KVKIKQKDTFGKMNALH <th>VLMSANPLDNNNGIEGAFEGVT</th> <th>FHIRIAEAKLTSVPKGLPP 240</th>	VLMSANPLDNNNGIEGAFEGVT	FHIRIAEAKLTSVPKGLPP 240
DB	175	KVKIKQKDTFGKMNALH <th>VLMSANPLENNIEGAFEGVT</th> <th>FHIRIAEAKLTSIPKGLPP 234</th>	VLMSANPLENNIEGAFEGVT	FHIRIAEAKLTSIPKGLPP 234
QY	241	TLLELHDYNNKISTVELE <th>DFKRYEQLORGLGNNKITT</th> <th>DIENGLSNIAPRVREIHLNNKL 300</th>	DFKRYEQLORGLGNNKITT	DIENGLSNIAPRVREIHLNNKL 300
DB	235	TLLELHDYNNKISTVELE <th>DFKRYEQLORGLGNNKITT</th> <th>DIENGLSNIAPRVREIHLNNKL 294</th>	DFKRYEQLORGLGNNKITT	DIENGLSNIAPRVREIHLNNKL 294
QY	301	KKIPSGLPKLYLOIIF <th>LHNSIARVGVDNFCPTVPKMKKSLYS</th> <th>SAISLFFNNPVKYWMOP 360</th>	LHNSIARVGVDNFCPTVPKMKKSLYS	SAISLFFNNPVKYWMOP 360
DB	295	KKIPSGLQELKLYLOI <th>IFLHNSIAKVGVDNFCPTVPKMKKSLYS</th> <th>SAISLFFNNPMKYWELQP 354</th>	IFLHNSIAKVGVDNFCPTVPKMKKSLYS	SAISLFFNNPMKYWELQP 354
QY	361	ATFRCVLSRMSVOLQNEG	378	
DB	355	ATFRCVLGRMSVOLQNGV	372	

PGSL_XENLA	ID	PGSL_XENLA	STANDARD;	PRT;	368 AA.
AC	Q9IBV5;				
DT	15-JUN-2002	(Rel. 41, Created)			
DT	15-JUN-2002	(Rel. 41, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Biglycan precursor.				
GN	BGN				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;				
OX	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RP	[1]				
RN	SEQUENCE FROM N.A.				
RA	Goto T., Kubota H.Y.;				
RT	*cDNA of biglycan of Xenopus laevis.*;				
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: May be involved in collagen fiber assembly (By similarity).				
CC	-1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRPS) FAMILY. CLASS 1 SUBFAMILY.				
CC	-1- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).				

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CC -----
DR EMBL: AB037269; BAA90246.1; -
DR InterPro: IPR001611; LRR_Nterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00560; LRR; 9.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00370; LRR; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19
FT PROPEP 20 ?
FT CHAIN 63 ? 368
FT DOMAIN 82 102
FT REPEAT 82 102
FT REPEAT 103 126
FT REPEAT 127 150
FT REPEAT 151 171
FT REPEAT 172 195
FT REPEAT 196 220
FT REPEAT 221 241
FT REPEAT 242 265
FT REPEAT 266 289
FT REPEAT 290 312
FT REPEAT 313 342
FT REPEAT 343 368
FT REPEAT 369 392
FT DISULFID 63 76
FT DISULFID 321 354
SQ SEQUENCE 368 AA; 41197 MW; 53ADF7E7E3BDC528 CRC64;

Query Match 52.4%; Score 1044; DB 1; Length 368;
Best Local Similarity 58.1%; Pred. No. 3.3e-65;
Matches 193; Conservative 61; Mismatches 72; Indels 6; Gaps 3;

QY 49 DEDNSL--FPTRE--PRGHFFPDLFPMCPGCCYSRVHCHSDGLTSPVTNIPFDTRM 105
Db 38 DEASGVGPPTESIPDVGLPMDL--CPGCGCHLRVQVCSGLTSPKPLPKDTTL 94
QY 106 LDQNNKKEIKENDFKGLTSLYLGLNNKLTIKHPKAFITTKRLRLYLHSHQLSEIP 165
Db 95 LDQNNKITEIKKDFKGLTSLYLGLNNKLTIKHPKAFITTKRLRLYLHSHQLSEIP 154
QY 166 LNLPSLAELRIHENKVKIKQDKFKGNALHVLMSANPLDNNNGIECPAEGVTVEHIR 225
Db 155 KNLPSLVELRLIHENKIKKVPKGVSGKLNKNCNTEMGNPLNGGIEAGAFDGLKLYLR 214
QY 226 TAAKLTSPKGLPPTLLEHLHDYDKNSTVELEDPKRYKELQRLGLGNKNTIDTENGSLA 285
Db 215 VSEAKLSGIPKGLPSTLNELHLDNNKIQAEKEDLSQVASYRLGLGHNNTRMTENGSLA 274
QY 286 NTPRVREHLENNKLTSPKGLPELKYLIQILFLHSNSTARVGVNDFCPVPMKKSLYSA 345
Db 275 FMPVLEHLDNNKLTSPKGLPELKYLIQILFLHSNSTARVGVNDFCPVPMKKSLYSA 334
QY 346 ISLFNNPKYVEMQATPCRCVLSRMSVOLGNF 377
Db 335 ISLFNNPKYVEMQATPCRCVLSRMSVOLGNF 366

RESULT 4
PGSI_RAT STANDARD; PRT; 369 AA.
AC P47853;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
GN BGN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX TISSUE=Vascular smooth muscle;
RA MEDLINE=91184222; PubMed=2081545;
RA Dreher K.L., Asundi V.K., Matzura D., Cowan K.;
RT "Vascular smooth muscle biglycan represents a highly conserved
RT proteoglycan within the arterial wall.";
RL Eur. J. Cell Biol. 53:296-304(1990).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY, CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: U17834; AAA58797.1; -
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR003592; LRR_Out.
CC InterPro: IPR003591; LRR_Typ.
CC Pfam: PF00560; LRR; 8.
CC Pfam: PF01462; LRRNT; 1.
CC SMART: SM00370; LRR; 3.
CC SMART: SM00013; LRRNT; 1.
CC SMART: SM00369; LRR_Typ; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19
FT PROPEP 20 37
FT CHAIN 38 369
FT DOMAIN 64 77
FT REPEAT 83 103
FT REPEAT 104 127
FT REPEAT 128 151
FT REPEAT 152 172
FT REPEAT 173 196
FT REPEAT 197 221
FT REPEAT 222 242
FT REPEAT 243 266
FT REPEAT 267 290
FT REPEAT 291 313
FT REPEAT 314 343
FT REPEAT 344 369
FT CARBOHYD 42 42
FT CARBOHYD 48 48
FT CARBOHYD 271 271
FT CARBOHYD 312 312
FT DISULFID 64 77
FT DISULFID 322 355
SQ SEQUENCE 369 AA; 41706 MW; 319DC15117F2C604 CRC64;

Query Match 52.2%; Score 1040.5; DB 1; Length 369;
Best Local Similarity 52.6%; Pred. No. 5.7e-65;
Matches 199; Conservative 67; Mismatches 93; Indels 19; Gaps 3;
```

```

QY 4 YVLLFLALCSAKPF-----FSPSHIALKNMMLKOWEDTDDDDDDDDDDDDDDDDDDNSLPFTR 59
DB 5 WLLTLLALLSALPFEQKGFWDFTLDDGLLMMNDEEASGSDTTSVDPDL-----SLTPT- 59
QY 60 EPRSHFFPDLFPMPFCQCYSRVHCSDLGLTSVPTNIPFDTRMLDQNNKKEIKEN 119
DB 60 -----FSAMCPFGCHLRVQCSDLGLTVKPEISPDFTLDDQNNDSLRKD 109
QY 120 DFKGLTSLYGLILNANNKLTIKHPKAFLTTRKRLYLKLNQSLSEIPNPKSLAEIRHE 179
DB 110 DFKGLHLYALVLYNNKISKIHERAFSPRLKQKLYISKHNLVEIPNLSLVELRIHD 169
QY 180 NKVKIKDKTEFGKGNALVLEMSANPDNNGIEPAGFEGVTVFHIRAEAKLTSVPKGLP 239
DB 170 NRIRKVPFGVSGLRNNNCIEMGNPNLENSGFEPGAFDGLKLNLYRTSEAKLTGPKDLP 229
QY 240 PTLELHLDYNKISTVELEDFKRYKELQRLGLGNKTKTDIENGSLANIIPRVREHLNKK 299
DB 230 ETNELHLDHKNKIQAELEDLLRYSKLYRLGLGHQIQRMTENGSLPFLRELHLDNNK 289
QY 300 LKKTIPSGLPKLYLOITILHNSNSTARVGNDFCTVTPKMKKSLYSALSIFNPNPKVWEMQ 359
DB 290 LSRVPAGLPDLKLVYLLHNSNITKVGINDFCMPGFKVRRYNGISLFPNPNVPYWEVQ 349
QY 360 PATRCVLSRMSVOLGNF 377
DB 350 PATRCVTDRLAIQFGNY 367

RESULT 5
PGS1_MOUSE STANDARD; PRT; 369 AA.
AC P28653; Q61355;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan 1) (PG-S1).
GN BGN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss; TISSUE=Fibroblast;
RC Naotoh Y., Suzuki S.;
RN Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss; TISSUE=Embryo;
RC MEDLINE=94319093; PubMed=8043960;
RA Rau W., Just W., Vetter U., Vogel W.;
RT "A dinucleotide repeat in the mouse biglycan gene (EST) on the X
RT chromosome.";
RL Mamm. Genome 5:395-396(1994).
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Breast, and Kidney;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE OF 11-152 FROM N.A.
RC STRAIN=C57BL/6;
RC PubMed=11311118;
RA Saegemaenen A.-M.K., Salminen H.J., Rantakokko A.J., Heinigaard D.,
RA Vuorio E.I.;
RT "Murine fibromodulin: cDNA and genomic structure, and age-related
RT expression and distribution in the knee joint.";
RL Biochem. J. 355:577-585(2001).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially

```

```

CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRPS) FAMILY, CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X53928; CAA37875.1; -
CC EMBL; U20276; AAA64360.1; -
CC EMBL; BC005452; AAH05452.1; -
CC EMBL; BC019502; AAH19502.1; -
CC EMBL; Y11758; CAA72422.1; -
CC PIR; S20811; S20811.
CC MGD; MGI:88158; Bgn.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003592; LRR_Out.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 8.
CC Pfam; PF01462; LRRNT; 1.
CC SMART; SM00370; LRR; 3.
CC SMART; SM00013; LRRNT; 1.
CC SMART; SM00369; LRR_Typ; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat:
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19
FT PROPEP 20 37
FT CHAIN 38 369
FT DOMAIN 64 77
FT REPEAT 83 103
FT REPEAT 104 127
FT REPEAT 128 151
FT REPEAT 152 172
FT REPEAT 173 196
FT REPEAT 197 221
FT REPEAT 222 242
FT REPEAT 243 266
FT REPEAT 267 290
FT REPEAT 291 313
FT REPEAT 314 343
FT REPEAT 344 369
FT CARBOHYD 42 42
FT CARBOHYD 48 48
FT CARBOHYD 271 271
FT CARBOHYD 312 312
FT DISULFID 64 77
FT DISULFID 322 355
FT CONFLICT 68 68
SQ SEQUENCE 369 AA; 41639 MW; 4B57FCC9A1026BE6 CRC64;
O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
C -> W (IN REF. 2).
Query Match 52.1%; Score 1037.5; DB 1; Length 369;
Best Local Similarity 52.4%; Pred. No. 9.2e-65;
Matches 198; Conservative 68; Mismatches 93; Indels 19; Gaps 3;
QY 4 YVLLFLALCSAKPF-----FSPSHIALKNMMLKOWEDTDDDDDDDDDDDDDDDDDDNSLPFTR 59
DB 5 WLLTLLALLSALPFEQKGFWDFTLDDGLLMMNDEEASGSDTTSVDPDL-----SLTPT- 59
QY 60 EPRSHFFPDLFPMPFCQCYSRVHCSDLGLTSVPTNIPFDTRMLDQNNKKEIKEN 119
DB 60 -----FSAMCPFGCHLRVQCSDLGLTVKPEISPDFTLDDQNNDSLRKD 109
QY 120 DFKGLTSLYGLILNANNKLTIKHPKAFLTTRKRLYLKLNQSLSEIPNPKSLAEIRHE 179

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Db 110 DFKGLHLYALVNNKISKTHKAFSPRLKQLYTSKNHLVPEIPNLPSSUVELRIHD 169
Qy 180 NKVKIKQIDTFKGMNALHVLMSANPLDNGIEPCAFEGVTVFIRIAEAKLTSPVKGGLP 239
Db 170 NKIRKVPKVSGLRNMNCIEMGNFLENSGFECAPDGLNLYRISEAKLTGIPKDLPL 229
Qy 240 PTLLEHLHDYKNKISTVELEDPKRYKELQRLGLGNKKTPTDIENGSLANIIPRVREIHLNNK 299
Db 230 ETLNELHLDHKNKIQATELEDLRLYSKLYRLGLGHQIRMIENGSLSFPLTRELHLDNNK 289
Qy 300 LKKIPSGIPELKYLQIIFLHNSIARVNDPCPTVPKMKKSLYSATSLFNPNPKYWEQ 359
Db 290 LSRVAGLQDLKQLVYLHNSNITKVGINDPCPMGFVGRKRAYNGISLFNPNPKYWEQ 349
Qy 360 PATFRCLVLSRMSVQLGNF 377
Db 350 PATFRCLVLSRMSVQLGNF 367

RESULT 6
PGSL_HUMAN STANDARD; PRT; 368 AA.
P21810: P13247;
D1 01-JAN-1990 (Rel. 13, Created)
D1 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
GN - BGN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN - [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=89174714; PubMed=2647739;
RA Fisher L.W., Termine J.D., Young M.F.;
RT "Deduced protein sequence of bone small proteoglycan I (biglycan)
RT shows homology with proteoglycan II (decorin) and several
RT nonconnective tissue proteins in a variety of species.";
RL J. Biol. Chem. 264:4571-4576(1989).
RN - [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91317791; PubMed=1860845;
RA Fisher L.W., Heegaard A.M., Vetter U., Vogel W., Just W.,
RA Termine J.D., Young M.F.;
RT "Human biglycan gene. Putative promoter, intron-exon junctions, and
RT chromosomal localization.";
RL J. Biol. Chem. 266:14371-14377(1991).
RN - [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20314869; PubMed=10854409;
RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
RA Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
RA Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K.,
RA Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,
RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man.";
RL Genome Res. 10:758-775(2000).
RN - [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN - [5]
RP SEQUENCE OF 38-57.
RX MEDLINE=90073579; PubMed=2590169;
RA Roughley P.J., White R.J.;
RT "Dermatan sulphate proteoglycans of human articular cartilage. The
RT properties of dermatan sulphate proteoglycans I and II.";
```

```
RL Biochem. J. 262:823-827(1989).
RN [6]
RP SEQUENCE OF 38-66.
RX MEDLINE=87250639; PubMed=3597437;
RA Fisher L.W., Hawkins G.R., Turos N., Termine J.D.;
RT "Purification and partial characterization of small proteoglycans I
RT and II, bone sialoproteins I and II, and osteonectin from the mineral
RT compartment of developing human bone.";
RL J. Biol. Chem. 262:9702-9708(1987).
RN [7]
RP SEQUENCE OF 361-368 FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=95187185; PubMed=7881444;
RA Just W., Rau W., Muller R., Georkens C., Vogel W.;
RT "Dinucleotide repeat polymorphism at the human biglycan (BGN)
RT locus.";
RL Hum. Mol. Genet. 3:2268-2268(1994).
CC -I- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -I- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -I- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -I- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -I- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY, CLASS I SUBFAMILY.
CC -I- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04599; AAA36009.1; -
DR EMBL; M65153; AAA52287.1; ALT_SEQ.
DR EMBL; M65152; AAA52287.1; JOINED.
DR EMBL; U82695; AAF3530.1; -
DR EMBL; BC002416; AAH02416.1; -
DR EMBL; BC004244; AAH04244.1; -
DR EMBL; U11686; AAC50117.1; -
DR PIR; A28457; A28457.
DR PIR; A32458; A32458.
DR PIR; A40757; A40757.
DR PIR; S05639; S05639.
DR Genew; HGNC:1044; BGN.
DR MIM; 301870; -
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19
FT PROPEP 20 37
FT CHAIN 38 368
FT DOMAIN 63 76
FT REPEAT 82 102
FT REPEAT 103 126
FT REPEAT 127 150
FT REPEAT 151 171
FT REPEAT 172 195
FT REPEAT 196 220
FT REPEAT 221 241
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[illegible]

RESULT	7	PGSL_HORSE	STANDARD;	PRT;	372 AA.
ID	PGSL_HORSE	STANDARD;	PRT;	372 AA.	
AC	046403;	09NIU5;			
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DE	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Biglycan precursor	(Bone/cartilage proteoglycan I) (PG-SI).			
GN	BGN.				
OS	Equus caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
OX	NCBI_TaxID=9796;				
[1]					
SEQUENCE FROM N.A.					
Richardson D.W., Dodge G.R.;					
"Dose dependent effects of corticosteroids on the expression of matrix					
related genes in equine articular chondrocytes.";					
Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.					
[2]					
SEQUENCE OF 150-192 FROM N.A.					
MEDLINE=20082971; PubMed=10613847;					
Caetano A.R., Shlue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,					
Bowling A.T., Murray J.D.;					
"A comparative gene map of the horse (Equus caballus).";					

```

Genome Res. 9:1239-1249(1999).
-!- FUNCTION: May be involved in collagen fiber assembly (By
similarity).
-!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
similarity).
-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-!- PMW: The two attached glycosaminoglycan chains can be either
chondroitin sulfate or dermatan sulfate (By similarity).
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
(SLRPs) FAMILY. CLASS 1 SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
-----
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-----
EMBL; AF035934; AAB88305.1; -
EMBL; AF135020; AAF64248.1; -
InterPro: IPR001611; LRR.
InterPro: IPR003072; LRR_Nterm.
InterPro: IPR003592; LRR_Out.
InterPro: IPR003591; LRR_Typ.
Pfam; PF00560; LRR; 7.
Pfam; PF01462; LRRNT; 1.
SMART; SM00370; LRR; 3.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_Typ; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
KW SIGNAL
FT 1 22 POTENTIAL
FT PROPEP 23 40 BY SIMILARITY.
FT CHAIN 41 372 BIGLYCAN.
FT DOMAIN 67 80 CYS-RICH.
FT REPEAT 86 106 LRR-S 1.
FT REPEAT 107 130 LRR-T 1.
FT REPEAT 131 154 LRR-T 2.
FT REPEAT 155 175 LRR-S 2.
FT REPEAT 176 199 LRR-T 3.
FT REPEAT 200 224 LRR-T 4.
FT REPEAT 225 245 LRR-S 3.
FT REPEAT 246 269 LRR-T 5.
FT REPEAT 270 293 LRR-T 6.
FT REPEAT 294 316 LRR-S 4.
FT REPEAT 317 346 LRR-T 7.
FT REPEAT 347 372 LRR-T 8.
FT CARBOHYD 45 45 O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
FT CARBOHYD 51 51 O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 67 80 BY SIMILARITY.
FT DISULFID 325 358 BY SIMILARITY.
SQ SEQUENCE 372 AA; 41924 MW; DOBBF8576C5F082E CRC64;
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Query Match 51.6%; Score 1028.5; DB 1; Length 372;
Best Local Similarity 52.4%; Pred. No. 3.9e-64;
Matches 198; Conservative 67; Mismatches 94; Indels 19; Gaps 3;

QY 4 YVLLFLALCAKPF-----FSPSHIALKNMMLKDWDTDDDDDDDDDDDDDDSLFPTR 59
:: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 WLLASLLALSOALPEQKGFWDFTLDGLPLMNDDEASGADTSGIPDL----SLTPT- 62

QY 60 EPRSHFFPDLPFMCFFGCQCYSRVHVCSDGLTTSVPTNIPDFTMLDLQNNKIKETKEN 119
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 -----FSAMCPFGCHLRVVCQSDGLKAVPKELSPDITLLDLQNNELSELKRD 112

QY 120 DFKGLTSLYGLLNNKLTIKHPKAFLTTKKLRRLYLSHNNOLSEIPLNPKSLAEIRHE 179
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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CC	EMBL: AF034842; AAB87988.1; -	
DR	InterPro: IPR001611; LRR	
DR	InterPro: IPR000372; LRR_Nterm.	
DR	InterPro: IPR003592; LRR_Out.	
DR	InterPro: IPR003591; LRR_typ.	
DR	pfam: PF00560; LRR: 7	
DR	pfam: PF01462; LRRNT: 1.	
DR	SMART: SM00370; LRR: 3.	
DR	SMART: SM00013; LRRNT: 1.	
DR	SMART: SM00369; LRR_TYP: 1.	
KW	Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;	
KW	Leucine-rich repeat; Signal.	
FT	SIGNAL 1 19	POTENTIAL.
FT	PROPEP 20 37	BY SIMILARITY.

AC	002678;	
DDT	15-JUL-1998 (Rel. 36, Created)	
DT	15-JUL-1998 (Rel. 36, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).	
DE	Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).	
GN	BGN.	
GN	Canis familiaris (Dog)	
OC	Canis familiaris (Dog)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX	NCBI_TaxID=9615;	
OX	[1]	
RN	SEQUENCE FROM N.A.	
RP	Glant T.T.;	
RA		

```

Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in collagen fiber assembly (By
similarity).
-!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
similarity).
-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-!- PMW: The two attached glycosaminoglycan chains can be either
chondroitin sulfate or dermatan sulfate (By similarity).
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
(SLRPS) FAMILY. CLASS I SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).

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EMBL; U83140; AAB51244.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_Out.
InterPro; IPR003591; LRR_type.
Pfam; PF00560; LRR_7.
Pfam; PF01462; LRRNT; 1.
SMART; SM00370; LRR; 3.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_type; 1.
Glycoprotein; Extracellular matrix;
Leucine-rich repeat; Signal.
Proteoglycan; Repeat;

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SIGNAL	1	19	POTENTIAL.
PROPEP	20	37	BY SIMILARITY.
CHAIN	38	369	BIGLYCAN.
DOMAIN	64	77	CYS-RICH.
REPEAT	83	103	LRR-S 1.
REPEAT	104	127	LRR-T 1.
REPEAT	128	151	LRR-T 2.
REPEAT	152	172	LRR-S 2.
REPEAT	173	196	LRR-T 3.
REPEAT	197	221	LRR-T 4.
REPEAT	222	242	LRR-S 3.
REPEAT	243	266	LRR-T 5.
REPEAT	267	290	LRR-T 6.
REPEAT	291	313	LRR-S 4.
REPEAT	314	343	LRR-T 7.
REPEAT	344	369	LRR-T 8.
CARBOHYD	42	42	O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
CARBOHYD	48	48	O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
CARBOHYD	271	271	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	312	312	N-LINKED (GLCNAC. . .) (POTENTIAL).
DISULFID	64	77	BY SIMILARITY.
DISULFID	322	355	BY SIMILARITY.
SEQUENCE	369 AA;	41566 MW;	8C919E922D6377E6 CRC64;

```

Query Match          51.3%:  Score 1021.5;  DB 1;  Length 369;
Best Local Similarity 51.6%:  Pred. No. 1.2e-63;
Matches 195;  Conservative 68;  Mismatches 96;  Indels 19;  Gaps 3;

Y 4 YVLLFLALCSAKPFPSHIALKNMMLKMDTDDDD---DDDDDDDDDSLSLPTTR 59
   :::  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
b 5 WLVASLLALSQLAPTEQ-----KGFWDTLDGLFLMUNDEEASGAETTSVPDL 53
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Y 60 EPRSHFFPFDLEPMCFGCQCYRVRVHCHSDGLGTSVPTNIPFOTRMLDLONNNKI 119
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 54 DALTPTYS-----AMCFGCCHLVRVVGQSDGLGKAVPKESPTMTLMDLQNNDIS 109
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Y 120 DFKGLTSLYGLLNNKLTKIHPRAFLTTKRLRYLYSHNOLSEIPLNPKSLAEIRIHE 179
   |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
b 110 DFKGLHLLYALVNVNKTSTKEKAFSPRLKQLXYTSKNHLYVEIPNTPSSLYELRIHD 169
   |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

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QY	180	NKVKKIQKDTFGKMNALHVLSEANPLDNNNGIEPGAEGVTVFHIRTAEAKLTSPVKGLP	233
Db	170	NRIRVPKGVTSGLRNMNCIEMGNGNPLENSCFEPAFDGLKLNYLRISAEAKLTGICPKDL	229
QY	240	PITLLEHLHDYHKISTVELEDPKRYKELORGLGNKNKTDTENGSLANIPIKVRHIHLNNK	299
Db	230	EFTNELHLDHNKIKQAIIEEDLLRSKYRLGLGHQNRIMLENGLSFLPTLREHLDDNK	289
QY	300	LKKIPSGLPKLKIQLTIIFLHSNSTARVGNDCEFTCPFKMKKSILYSATSLFNPNPVKYWEQ	359
Db	290	LSRVPSGLPDCLKLOVVYLHTFNNTIKVGVDNFCVGFVGRAYYINGISLFNNPVPVYEVO	349
QY	360	PATRCVLSRMSVOLGNF	377
Db	350	PATERCVTRLAQFGNY	367
 RESULT 10 PGSL_BOVIN			
ID	PGSL_BOVIN	STANDARD;	PRT; 369 AA.
AC	P21809;		
DT	01-MAY-1991 (Rel. 18, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Biglycan precursor (Bone/cartilage proteoglycan I) (PG-SI) (Leucine-rich PG I).		
DE	BGN.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Aorta;		
RX	MEDLINE=96113563; PubMed=8673009;		
RA	Xu J.H., Radhakrishnamurthy B., Srinivasan S.R., Berenson G.S.;		
RT	"Primary structure of bovine aorta biglycan core protein deduced from cloned cDNA."		
RL	Biochem. Mol. Biol. Int. 37:263-272(1995).		
RN	[2]		
RP	SEQUENCE OF 38-69.		
RC	TISSUE=Cartilage;		
RX	MEDLINE=89255324; PubMed=2656687;		
RA	Neame P.J., Choi H.U., Rosenberg L.C.;		
RT	"The primary structure of the core protein of the small, leucine-rich proteoglycan (PG I) from bovine articular cartilage."		
RL	J. Biol. Chem. 264:8653-8661(1989).		
RN	[3]		
RP	SEQUENCE OF 38-63.		
RC	TISSUE=Cartilage;		
RX	MEDLINE=89123388; PubMed=2914936;		
RA	Choi H.O., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C., Neame P.J.;		
RT	"Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, from bovine articular cartilage and skin isolated by octyl-sepharose chromatography."		
RL	J. Biol. Chem. 264:2876-2884(1989).		
RN	[4]		
RP	INTERACTIONS WITH MFAP2 AND ELN.		
RA	Reinboth B., Hanssen E., Cleary E.G., Gibson M.A.;		
RT	"Molecular interactions of biglycan and decorin with elastic fiber components: biglycan forms a ternary complex with tropoelastin and microfibril-associated glycoprotein 1;"		
RL	J. Biol. Chem. 277:3950-3957(2002).		
CC	-!- FUNCTION: May be involved in collagen fiber assembly.		
CC	-!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN.		
CC	-!- SUBCELLULAR LOCATION: Extracellular matrix.		
CC	-!- TISSUE SPECIFICITY: Found in several connective tissues, specially in articular cartilages.		
CC	-!- PTM: The two attached glycosaminoglycan chains can be either		

Query Match	51.2%	Score 1019.5	DB 1	Length 369
Best Local Similarity	51.9%	Pred. No. 1.6e-63		
Matches 195	Conservative 65	Mismatches 97	Indels 19	Gaps 3
6	LLLEALCSNKKPFSSHTALKNMMLKDMEDTDDDD	-----DDDDDDDDDD	SLREP	61
7	LAALLAASQALPEEQ	-----KATWFTLDDGLPMLNDEASCAETTS	GCIPDLDS	55
62	RSHPFFDLFPMPFCQCYSRVHCSDLGLTSVPNNIFDTRMLDLQNNKTKKEKENDF	121		
56	----LPPTYSAMCPFGCHLRVRVQCSDLGLKAVPKIESPDTTLTDLQNNDISELRKDDF	111		
122	KGLTSLYGLLNNKNTKIHPKAFLTTKTLRLRLYLSHNSQISPIPLNPKSLAELRIHENK	181		
112	KGLOHLYALVLVNNKISKIIEKAFSPRLKQKIYISKNHLCETPPMLPSSLVELRIHDNR	171		
182	VKKIQKDTDFKGMNALHVLEMSANPLDNNNGIEPCAFSGVTVFHRIRAEALTSVPKGLPT	241		
172	IPKVKCVFCSLENNACIFWCGNPIENSCFPCAFDGLKINLYIRISEAKITGLPKDLPT	231		



```

Db 103 KNLHALILVNNKISKTSFAAFAPLKKLELYLSKNKLKELPENMPKSLQETRAHENEISK 162
QY 185 IOKDTFGKGNALHVLMSANPLDNNNGIEPCAFEGV-TVFHRIAEAKLTSPKGLPPTIL 243
Db 163 LRKAVENGLNOVIVLEGTNPPLKSSGIENGAFQGMKRLSYRIADNTITSIPKGLPPSLT 222
QY 244 ELHLDYKNTSTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNKLKKI 303
Db 223 ELHLDGKNKSIDAEGSLGTLNLAKLGLSFNSTSSVENGSLNNVPHRLHLLNNELVRV 282
QY 304 PSGLPKLYLQIIFLHNSNSTARVGVNDPCTVPKMKKSLYSALSFNPNVYKWEQPAIF 363
Db 283 PSGLGEHKYIQVYVYHNNKIATIGINDCPGLGYNTKRTATYSGVSLFSPNPVQIWEIQPSAF 342
QY 364 RCVLSRMSVOLGNF 377
Db 343 RCTHERSAVOIGNY 356

RESULT 13
PGS2_PIG STANDARD: PRT: 360 AA.
QXSD9: Q9XSH4;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
GN DGN.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A. (LONG ISOFORM).
STRAIN=Yorkshire;
RA Stephenson S., Schnoke M., Vesely I.;
RT "Cloning of the porcine decorin gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A. (SHORT ISOFORM).
STRAIN=Yorkshire; TISSUE=Aorta;
RA Stephenson S., Schnoke M., Vesely I.;
RT "Alternatively spliced version of the porcine decorin gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here)
CC and a short form; are produced by alternative splicing.
CC -!- PM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SURPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF125537; AAD23578.1;
CC EMBL; AF140270; AAD33862.1;
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003592; LRR_out.

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DR InterPro: IPR003591; LRR_type.
DR Pfam; PF00560; LRR; 7.
DR Pfam; PF01482; LRRNT; 1.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR-TYP; 2.
KW Glycoprotein; Extracellular matrix; proteoglycan; Repeat;
KW Leucine-rich repeat; Signal; Alternative splicing.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 314 347
FT CARBOHYD 34 34
FT CARBOHYD 212 212
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT VARSPLIC 281 318
FT VARSPLIC 281 318
SQ SEQUENCE 360 AA; 39899 MW; 8573DE8DDEBA7509 CRC64;

Query Match 48.5%; Score 967; DB 1; Length 360;
Best Local Similarity 50.9%; Pred. No. 6.6e-60;
Matches 193; Conservative 63; Mismatches 101; Indels 22; Gaps 5;

QY 1 MKEYVILLFLALCS-AKPFPSHIALNMMLKMDTDDDDDDDDDDDDDDDDDDDDSLFTR 59
Db 1 MKATIVFLLLAQVSWAGPF---QQKGLDFMLEASGIGPEDREPE-----VPEL 48
QY 60 EPRSHFFPDLFPMCFPCOCYSRVVHCSDLGTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
Db 49 EP-----LQPMCFPCQCHLRVQVQSDGLGDKVDPDLPDPTALLDLQNNKITEIDG 100
QY 120 DFKGLTSLYGLILNKKTKIHPKAFITTKLRLRYLSHNQSLSEIPLNLPKSLAELRIHE 179
Db 101 DFKNLKLNHTLILNKKISKISPGAFAPLVKLERLYLSKNQLKELPEKMPKTLQELRVE 160
QY 180 NKVKKTKQDTEKGMNALHYLEMSANPLDNNNGIEPCAFEGV-TVFHRIAEAKLTSPKGL 238
Db 161 NEITKYRKAFFNGLNOMIVVELGTNPLKSSGIENGAFQGMKRLSYRIADNTITTIPOGL 220
QY 239 PPTLLEHLDYKNTSTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIPRVREIHLNEN 298
Db 221 PPSLTLEHLDGKNKISKVDAASLKLGNLAKLGLGFNSTSTVDGSLANTPHLREHLNEN 280
QY 299 KLKIPSGLPKLYLQIIFLHNSNSTARVGVNDPCTVPKMKKSLYSALSFNPNVYKWE 358
Db 281 KLNKVPGLAEHKYIQVYVYHNNKIATIGINDCPGLGYNTKRTATYSGVSLFSPNPVQIWEI 340
QY 359 QPATFRVLSRMSVOLGNF 377
Db 341 QPSTFRVYVYSAIQLGNY 359

RESULT 14
PGS2_HUMAN STANDARD: PRT: 359 AA.
ID PGS2_HUMAN
AC P07585; Q9Y5N9; Q9Y5N8; Q9P020; Q9P021;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)

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RESULT 15

PGS2_SHEEP	STANDARD:	PRT:	360 AA.
ID	PGS2_SHEEP		
AC	Q9TTE2;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).		
GN	DCN.		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Myometrium;		
RC	MEDLINE=20113292; PubMed=10644528;		
RA	Wu W.X., Zhang Q., Umno N., Derks J.B., Nathanielsz P.W.;		
RT	"Characterization of decorin mRNA in pregnant intrauterine tissues of the ewe and regulation by steroids.";		
RT	Am. J. Physiol. 278:C199-C206(2000).		
RL	-I- FUNCTION: May affect the rate of fibrils formation (By similarity).		
CC	-I- SUBUNIT: Binds to type I and type II collagen, to fibronectin and Tcf-beta. Forms a ternary complex with WFAP2 and ELN (By similarity).		
CC	-I- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).		
CC	-I- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).		
CC	-I- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.		
CC	-I- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).		
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		

Search completed: May 27, 2003, 16:04:27  
Job time : 16 secs

Query Match	47.5%;	Score 947;	DB 1;	Length 360;
Best Local Similarity	49.7%;	pred. No. 1.6e-58;		
Matches 100. Conservative	67;	Mismatches 97;	Indels 28;	Gaps 7;



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 27, 2003, 15:46:26 ; Search time 37 seconds  
(without alignments)  
1364.919 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFES.....PATRCVLRSVQLGNFCM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	379	21	AA01311
2	1992	100.0	379	22	AAU12335
3	1992	100.0	379	23	AB95437
4	1992	100.0	379	23	AB84831
5	1990	99.9	379	20	AA117820
6	1799	90.3	373	22	AAE05347
7	1799	90.3	373	23	AB872356
8	1649	82.8	344	22	AA40351
9	1558	78.2	352	22	ABG22569
10	1237	62.1	246	22	AA95678
					Human PRO241 polyp
					Human PRO241 polyp
					Human angiogenesis
					Human PRO241 prote
					Human PRO241 prote
					Mouse bone/cartila
					Murine protein iso
					Human polypeptide
					Novel human diagno
					Human protein sequ

11	1040.5	52.2	369	16	AA087951	Rat neurotrophic b
12	1034	51.9	368	22	AA085043	Human biglycan pro
13	1031.5	51.8	369	16	AA087952	Human neurotrophic
14	1021	51.3	368	22	AA0879510	Human biglycan ami
15	1020	51.2	368	11	AA085159	Sequence of human
16	1015	51.0	332	16	AA087953	Bovine neurotroph
17	1007	50.6	197	22	AA042137	Human polypeptide
18	963.5	48.4	359	21	AA057079	Human decorin amin
19	963.5	48.4	359	22	AA0879511	Human decorin amin
20	963.5	48.4	360	22	AA087286	Novel central nerv
21	949	47.6	342	17	AA089439	Human recombinant
22	947	47.5	331	14	AA042260	Mature decorin PT-
23	947	47.5	1388	17	AA089471	Collagen/decorin f
24	947	47.5	1388	21	AA084539	Amino acid sequenc
25	907	45.5	353	11	AA05160	Sequence of human
26	847	42.5	305	14	AA042267	Decorin sequence p
27	793.5	39.8	423	22	AA030348	Novel human secret
28	776	39.0	280	14	AA042266	Decorin sequence p
29	643	32.3	128	22	AA020404	Human secreted pro
30	616	30.9	234	14	AA042265	Decorin sequence p
31	493	24.7	88	21	AA000241	Human secreted pro
32	493	24.7	88	21	AA04720	Human 5' EST relat
33	493	24.7	186	14	AA042264	Decorin sequence p
34	433	21.7	146	20	AA059749	Human normal ovari
35	406.5	20.4	155	21	AA044116	Human cancer assoc
36	397.5	20.0	699	21	AA067598	Human adipose tiss
37	393	19.7	353	21	AA043535	Human cancer assoc
38	390	19.6	338	23	AB090763	Human Tumour Endot
39	390	19.6	353	22	AA073881	Human colon cancer
40	384.5	19.3	139	14	AA042263	Decorin sequence p
41	366	18.4	421	20	AA0505767	Human osteomodulin
42	366	18.4	421	21	AA033417	Human PRO216 prote
43	366	18.4	421	21	AA024435	Human PRO216 prote
44	366	18.4	421	21	AA088377	PRO216 (osteomodul
45	366	18.4	421	22	AAU12322	Human PRO216 polyp

## ALIGNMENTS

RESULT 1

AA01311

ID AA01311 standard; Protein: 379 AA.

AC AA01311;

XX

DT 25-SEP-2000 (first entry)

XX

DE Human PRO241 polypeptide.

XX

KW PRO; membrane bound protein; secreted protein; PRO357; PRO327;

KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO344; PRO347;

KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;

KW antibody; screening; detection; inhibition; probe; primer; human.

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT Peptide 1..15

FT Modified-site /label= Signal peptide

FT /note= "N-myristoylation site"

FT Domain 154..176

FT /label= Leucine zipper pattern

FT Modified-site 210..216

FT /note= "N-myristoylation site"

FT Modified-site 214..220

FT /note= "N-myristoylation site"

FT Modified-site 214..220

FT /note= "N-myristoylation site"

FT Modified-site 237..243

FT /note= "N-myristoylation site"

FT Modified-site 270..276

FT Modified-site /note= "N-myristoylation site"  
 FT 281..285  
 FT /note= "N-glycosylation site"  
 FT 282..288  
 FT /note= "N-myristoylation site"  
 XX  
 PN WO200032776-A2.  
 XX  
 PN 08-JUN-2000.  
 XX  
 PF 01-DEC-1999; 99WO-US28301.  
 XX  
 XX 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;  
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
 XX  
 XX WPI; 2000-412324/35.  
 XX N-PSDB; AAA49551.  
 XX  
 PT New human nucleic acids encoding secreted and transmembrane  
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical  
 PT and diagnostic agents  
 XX  
 PS Claim 12; Fig 2; 187pp; English.  
 XX  
 CC New human nucleic acids encoding secreted and transmembrane  
 CC polypeptides which are designated as PRO polypeptides are described  
 CC The membrane-bound proteins have various industrial applications,  
 CC including as pharmaceutical and diagnostic agents. The membrane-bound  
 CC proteins can also be employed for screening of potential peptide or  
 CC small molecule inhibitors of the relevant receptor/ligand interaction.  
 CC Anti-PRO antibodies are useful for the affinity purification of PRO  
 CC from recombinant cell culture or natural sources.  
 XX  
 SQ Sequence 379 AA;  
 Query Match 100.08; Score 1992; DB 21; Length 379;  
 Best Local Similarity 100.08; Pred. No. 4e-177;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 MKEYVLLFLALCSAKPFPSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60  
 61 PRSHFFPDLFPMCPGCGCYSRVVHCSDGLGTSVPTNIPFTRMLDLQNNKIKETKEND 120  
 61 PRSHFFPDLFPMCPGCGCYSRVVHCSDGLGTSVPTNIPFTRMLDLQNNKIKETKEND 120  
 QY 121 FKCLTSLYGLILNNKLTTHPKAFITTKKRLRLYLSHNSLSEIPLNLPKSLAEURLIHEN 180  
 DB 121 FKCLTSLYGLILNNKLTTHPKAFITTKKRLRLYLSHNSLSEIPLNLPKSLAEURLIHEN 180  
 QY 181 KVKIKQKDFKGMNALHVLMSANPLDNGIEGAFEGVTVFHIRIAEAKLTSPVKGLPP 240  
 DB 181 KVKIKQKDFKGMNALHVLMSANPLDNGIEGAFEGVTVFHIRIAEAKLTSPVKGLPP 240  
 QY 241 TLELHLDYNTKSTVELEDFKRYKELQRLGNNKITDIENGSLANIPRVREIHLNKL 300  
 DB 241 TLELHLDYNTKSTVELEDFKRYKELQRLGNNKITDIENGSLANIPRVREIHLNKL 300  
 QY 301 KKTPSGLPELKYLOIIFLHNSNTARVGVNDFCTVPKMKKSLYSALSFNPNPKYEMQP 360  
 DB 301 KKTPSGLPELKYLOIIFLHNSNTARVGVNDFCTVPKMKKSLYSALSFNPNPKYEMQP 360  
 QY 361 ATRFCVLSRMSVOLGNFGM 379  
 DB 361 ATRFCVLSRMSVOLGNFGM 379

## RESULT 2

AAU12335  
 ID AAU12335 standard; Protein; 379 AA.  
 XX  
 AC AAU12335;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO241 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 08-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03365.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR N-PSDB; AAS21407.  
 XX  
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
 other PRO polypeptides, link bioactive molecules to cells expressing  
 PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 lung, breast, prostate, cervical  
 PT  
 XX Claim 12; Fig 328; 813pp; English.  
 PS  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
 PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing



CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 379 AA;

Query Match 100.0%; Score 1992; DB 23; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 4e-177;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60

DB 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60

OY 61 PRSHFFPDLFPMCPFGCQYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120

DB 61 PRSHFFPDLFPMCPFGCQYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120

OY 121 FKGLTSLGLIILNNKLTKIHPKAFLLTKKRLRLYLSHNSLSEIPLNPKSLAELRIHEN 180

DB 121 FKGLTSLGLIILNNKLTKIHPKAFLLTKKRLRLYLSHNSLSEIPLNPKSLAELRIHEN 180

OY 181 KYKTKQDQFKGMALHVLNSANPLDNGIEPGAFEGTVFHRIARAKLTSVPKGLPP 240

DB 181 KYKTKQDQFKGMALHVLNSANPLDNGIEPGAFEGTVFHRIARAKLTSVPKGLPP 240

OY 241 TLELHLDYNTKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNKKL 300

DB 241 TLELHLDYNTKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNKKL 300

OY 301 KIPSGLPKLYLOIFLHNSIARVGNDCPTVPKMKKSLYSALSIFNPNVYEWMP 360

DB 301 KIPSGLPKLYLOIFLHNSIARVGNDCPTVPKMKKSLYSALSIFNPNVYEWMP 360

OY 361 ATRFVLSRMSVQLGNFGM 379

DB 361 ATRFVLSRMSVQLGNFGM 379

RESULT 4

ID ABB84831 standard; Protein; 379 AA.

AC ABB84831;

DT 16-MAY-2002 (first entry)

XX Human PRO241 protein sequence SEQ ID NO:30.

Human; angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;  
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23528.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 25-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.

(GETH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerecht H, Gerritsen ME, Goddard A;

Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;

WPI; 2002-090516/12.

N-PSDB; ABL88086.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 infarction), endothelial or angiogenic disorders in a mammal.

Claim 11; Fig 30; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,  
 antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 activities, and can be used in gene therapy. The PRO polynucleotides  
 proteins, agonists and antagonists are useful for treating or diagnosing  
 a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 degeneration, atherosclerosis, hypertension, arterial restenosis,  
 rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 carcinoma) and wound healing. The PRO polynucleotides have applications  
 in molecular biology, including use as hybridisation probes, and in  
 chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 probes used in the exemplification of the present invention.

Sequence 379 AA;

Query Match 100.0%; Score 1992; DB 23; Length 379;

Best Local Similarity 100.0%; Pred. No. 4e-177;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPPTRE 60

DB 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPPTRE 60

OY 61 PRSHFFPDLFPMCPFGCQYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120

Db 61 PRSHFFPDLFPMCPFGCOCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
 Qy 121 FKGLTSYGLILNNKLTTHPKAFLLTKLRRLYLSHNOLSEIPLNPKSLAELRIHEN 180  
 Db 121 FKGLTSYGLILNNKLTTHPKAFLLTKLRRLYLSHNOLSEIPLNPKSLAELRIHEN 180  
 Qy 181 KVKIKQDTEFGMNAHVLMSANPLDNGIEPGAFEGTVTFHRIAEAKLTSVPKGLPP 240  
 Db 181 KVKIKQDTEFGMNAHVLMSANPLDNGIEPGAFEGTVTFHRIAEAKLTSVPKGLPP 240  
 Qy 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 300  
 Db 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 300  
 Qy 301 KKIPSGLPKYLQIIFLHSNLSARVGNDFCPTVPKMKKSLYSALSLENPNPKYWEQMP 360  
 Db 301 KKIPSGLPKYLQIIFLHSNLSARVGNDFCPTVPKMKKSLYSALSLENPNPKYWEQMP 360  
 361 ATFCVLSRMSVOLGNFGM 379  
 361 ATFCVLSRMSVOLGNFGM 379

RESULT 5  
 AAY17820  
 .ID AAY17820 standard; Protein; 379 AA.  
 XX  
 AC AAY17820:  
 XX  
 DT 12-AUG-1999 (first entry)  
 XX  
 DE Human PRO241 protein sequence.  
 XX  
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;  
 secreted protein; transmembrane protein; inflammation disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9928462-A2.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 01-DEC-1998; 98WO-US25108.  
 XX  
 PR 25-FEB-1998; 98US-0075945.  
 03-DEC-1997; 97US-0067411.  
 11-DEC-1997; 97US-0069278.  
 11-DEC-1997; 97US-0069334.  
 11-DEC-1997; 97US-0069335.  
 12-DEC-1997; 97US-0069425.  
 16-DEC-1997; 97US-0069694.  
 16-DEC-1997; 97US-0069696.  
 16-DEC-1997; 97US-0069702.  
 17-DEC-1997; 97US-0069870.  
 17-DEC-1997; 97US-0069873.  
 18-DEC-1997; 97US-0068017.  
 05-JAN-1998; 98US-0070440.  
 09-FEB-1998; 98US-0074086.  
 09-FEB-1998; 98US-0074092.

(GETH ) GENENTECH INC.

Baker KP, Chen J, Goddard A, Gurney AL, Wood WT;  
 Yuan J;WPI; 1999-371118/31.  
 N-PSDB; AAX80043.

Nucleic acids encoding PRO secreted and transmembrane proteins

Claim 12; Fig 2; 123pp; English.

The present invention describes nucleic acids encoding PRO secreted and

CC transmembrane proteins used therapeutically. The PRO proteins have  
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive  
 CC activity. The proteins and polynucleotides can be used in therapy,  
 CC identification of homologues, raising antibodies and design of probes  
 CC and primers. They can be used in a range of diseases related to proteins  
 CC that they have homology with, e.g. a PRO protein having homology to  
 CC complement proteins may be used in inflammatory responses.

SQ Sequence 379 AA;

Query Match 99.9%; Score 1990; DB 20; Length 379;  
 Best Local Similarity 99.7%; Pred. No. 6.2e-177;  
 Matches 378; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKEYVLLLFALCSAKPFPSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60  
 Db 1 MKEYVLLLFALCSAKPFPSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60  
 Qy 61 PRSHFFPDLFPMCPFGCOCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
 Db 61 PRSHFFPDLFPMCPFGCOCYSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
 Qy 121 FKGLTSYGLILNNKLTTHPKAFLLTKLRRLYLSHNOLSEIPLNPKSLAELRIHEN 180  
 Db 121 FKGLTSYGLILNNKLTTHPKAFLLTKLRRLYLSHNOLSEIPLNPKSLAELRIHEN 180  
 Qy 181 KVKIKQDTEFGMNAHVLMSANPLDNGIEPGAFEGTVTFHRIAEAKLTSVPKGLPP 240  
 Db 181 KVKIKQDTEFGMNAHVLMSANPLDNGIEPGAFEGTVTFHRIAEAKLTSVPKGLPP 240  
 Qy 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 300  
 Db 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 300  
 Qy 301 KKIPSGLPKYLQIIFLHSNLSARVGNDFCPTVPKMKKSLYSALSLENPNPKYWEQMP 360  
 Db 301 KKIPSGLPKYLQIIFLHSNLSARVGNDFCPTVPKMKKSLYSALSLENPNPKYWEQMP 360  
 Qy 361 ATFCVLSRMSVOLGNFGM 379  
 Db 361 ATFCVLSRMSVOLGNFGM 379

RESULT 6

AAE05347

ID AAE05347 standard; Protein; 373 AA.

XX

AC AAE05347;

XX

DT 12-SEP-2001 (first entry)

XX Mouse bone/cartilage proteoglycan I (BGN) protein.

XX Mouse; cytostatic; antinflammatory; immunoregulatory; tissue integrity;  
 wound healing; immune response; vaccine; cancer; asthma; allergy;  
 cell trafficking; BGN; bone/cartilage proteoglycan I protein;  
 biglycan; PG-S1; secreted protein; therapy.

OS Mus sp.

XX

PN WO200148192-A1.

XX

PD 05-JUL-2001.

XX

PF 21-DEC-2000; 2000WO-NZ00256.

XX

PR 23-DEC-1999; 99US-0171678.

XX

PR 28-NOV-2000; 2000US-0724864.

XX

PA (GENE-) GENESIS RES &amp; DEV CORP LTD.

XX Watson JD, Murison JG;

XX

WPI: 2001-425665/45.  
N-PSDB: AAD10114.

Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target -

Claim 6: Page 76-77; 101pp; English.

The patent discloses novel polynucleotides and their corresponding proteins which play a major role in induction of growth, cell migration and proliferation, cell-cell interaction and the differentiation of tissue-specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise antibodies, to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of genes, to tag or identify an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response as part of a vaccine or anti-cancer treatment, as target for cancer treatment, as immunoregulatory and anti-inflammatory molecule, as diagnostic for specific types of cancer and for development of an anti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is bone/cartilage proteoglycan I (BGN) protein. A secreted protein from mouse. BGN is also known as biglycan or PG-S1.

Sequence 373 AA:

Query Match 90.3%; Score 1799; DB 22: Length 373;  
Best Local Similarity 90.2%; Pred. No. 3.9e-159;  
Matches 341; Conservative 17; Mismatches 14; Indels 6; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60  
DB 1 MKEYVLLLLAVCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPPTRE 54  
QY 61 PRSHFFPDLFPMPGCGQCYSRVHCHSDGLTSVPTNIPFDRMLDLQNNKIKEIKEND 120  
DB 55 PVNPFPPDLFPMPGCGQCYSRVHCHSDGLTSVPTNIPFDRMRVDLQNNKIKEIKEND 114  
121 FKGLTSLYLILNNKLTTHPKAFITTKKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 180  
115 FKGLTSLYALILNNKLTTHPKFTFTTKKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 174  
QY 181 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 240  
DB 175 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 234  
QY 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKTTDENGSLANIPRVREIHLNKKL 300  
DB 235 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKTTDENGSLANIPRVREIHLNKKL 294  
QY 301 KKIPLGPELKYLOITFLHSNSTARVGVNDCTVPMKSKSYLSAISLNNPKYVEMOP 360  
DB 295 KKIPLGPELKYLOITFLHSNSTARVGVNDCTVPMKSKSYLSAISLNNPKYVEMOP 354  
QY 361 ATPRCVLSRMSVOLGNFG 378  
DB 355 ATPRCVLSRMSVOLGNVG 372

RESULT 7  
ABB72356

ID ABB72356 standard; Protein: 373 AA.  
XX ABB72356;  
AC ABB72356;  
XX 04-APR-2002 (first entry)  
DT Murine protein isolated from skin cells SEQ ID NO: 680.  
XX  
DE Human; rat; mouse; skin cell; skin wound; cancer; growth defect;  
XX developmental defect; inflammatory disease; dermatological; vulnary;  
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.  
XX Mus sp.  
OS WC200190357-A1.  
XX  
PN 29-NOV-2001.  
XX  
PD 24-MAY-2001; 2001WO-NZ000099.  
XX  
PF 24-MAY-2000; 2000US-206650P.  
XX  
PR 25-JUL-2000; 2000US-221232P.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;  
PI WPI: 2002-122020/16.  
XX  
XX N-PSDB: ABL35045.  
DR  
XX New polynucleotides and polypeptides encoded by the polynucleotides  
PT isolated from skin cells, useful for treating skin wounds, cancers,  
PT growth and developmental defects, inflammatory diseases, or for  
PT modulating immune responses  
XX  
XX Claim 4; Page 434-435; 466pp; English.  
PS  
XX The present invention provides the protein and coding sequences of cDNAs  
CC isolated from human, murine and rat skin cell libraries. The sequences  
CC can be used in the development of therapeutic agents useful in the  
CC treatment of skin diseases, including skin wounds, cancer, growth  
CC defects, developmental defects and inflammatory diseases. The proteins  
CC have important roles in the induction of hair growth, cell proliferation  
CC and cell-cell interaction, in maintaining tissue integrity, in wound  
CC healing and in modulating immune responses. The present sequence is a  
CC polypeptide of the invention.  
XX  
SQ Sequence 373 AA;

Query Match 90.3%; Score 1799; DB 23: Length 373;  
Best Local Similarity 90.2%; Pred. No. 3.9e-159;  
Matches 341; Conservative 17; Mismatches 14; Indels 6; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPPTRE 60  
DB 1 MKEYVLLLLAVCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDNSLFPPTRE 54  
QY 61 PRSHFFPDLFPMPGCGQCYSRVHCHSDGLTSVPTNIPFDRMLDLQNNKIKEIKEND 120  
DB 55 PVNPFPPDLFPMPGCGQCYSRVHCHSDGLTSVPTNIPFDRMRVDLQNNKIKEIKEND 114  
QY 121 FKGLTSLYLILNNKLTTHPKAFITTKKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 180  
DB 115 FKGLTSLYALILNNKLTTHPKFTFTTKKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 174  
QY 181 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 240  
DB 175 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 234  
QY 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKTTDENGSLANIPRVREIHLNKKL 300  
DB 235 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKTTDENGSLANIPRVREIHLNKKL 294

QY 301 KKPSGLPELKYLIQIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNPNPVKYMWP 360  
 Db 295 KKPSGLQELKYLIQIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNPNPVKYMW 354  
 QY 361 ATRFVCLSRMSVOLGNFG 378  
 Db 355 ATRFVCLSRMSVOLGNVG 372

## RESULT 8

AA040351

ID AA040351 standard; Protein: 344 AA.

XX AA040351;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 3496.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-052317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 Zhao OA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AA159507.

XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -

XX Example 6; SEQ ID NO 3496; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AA038642-AA042213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

XX

SQ Sequence 344 AA;

Query Match 82.8%; Score 1649; DB 22; Length 344;  
 Best Local Similarity 97.5%; Pred. No. 3.3e-145;  
 Matches 316; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 56 FPTREPRSHFFPDLPMPGFCQCYSRVHVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKE 115

Db 21 FOESQEAIFFPDLPMPGFCQCYSRVHVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKE 80

QY 116 IKENDEKGLTSLYGLILNNKLTKEHPKAFLLTKKLRRLYLSHNLSEIPLNPKSLAEL 175

Db 81 IKENDEKGLTSLYGLILNNKLTKEHPKAFLLTKKLRRLYLSHNLSEIPLNPKSLAEL 140

QY 176 RIHENVKKIQDFTFGMMALHLEMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPV 235

Db 141 RIHENVKKIQDFTFGMMALHLEMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPV 200

QY 236 KGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKITDLENGSLANIPRVREIHL 295

Db 201 KGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKITDLENGSLANIPRVREIHL 260

QY 296 ENNKKLKIPSGLPPELKYLIQIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNPNVKY 355

Db 261 ENNKKLKIPSGLPPELKYLIQIFLHNSIARVGVNDPCPTVPKMKKSLYSALSIFNPNVKY 320

QY 356 WEMQPATFRCLVSRMSVOLGNFGM 379

Db 321 WEMQPATFRCLVSRMSVOLGNFGM 344

## RESULT 9

ABG22569

ID ABG22569 standard; Protein: 352 AA.

XX AC ABG22569;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22560.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS86756.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits and to assess  
 CC biodiversity -

XX Claim 20; SEQ ID No 52928; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 352 AA;

Query Match 78.2%; Score 1558; DB 22; Length 352;  
 Best Local Similarity 93.6%; Pred. No. 1.1e-136;  
 Matches 305; Conservative 3; Mismatches 16; Indels 2; Gaps 2;  
 QY 56 FPTREPRSHFFPDLFPMCPFCQCYSRVHCSDLGLTSVPTNIPFDTMLDLQNNKIKE 115  
 DB 27 FOEGEQAIFFFDLFPMCPFCQCYSRVHCSDLGLTSVPTNIPFDTMLDLQNNKIKE 86  
 QY 116 IKENDFKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSLSEIPLNPKSLAEL 175  
 DB 87 IKENDFKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSLSEIPLNPKSLAEL 146  
 QY 176 RIHENVKKIQKDTFGMMALHVLMSANPLDNN-GIEPGAF-EGVTVFHRIAEAKLTS 233  
 DB 147 RIHENVKKIQKDTFGMMALHVLMSANPLXXSMGIEPGAFXRCXSYRIAEAKLTS 206  
 QY 234 VPKGLPPTLLEHLHDYKNKISTVELEDFRYKELQRLGLGNKKTIDENGSLANIPRVREI 293  
 DB 207 VPKGLPPTLLEHLHDYKNKISTVELEDFRYKELQRLGLGNKKTIDENGSLANIPRVREI 266  
 QY 294 HLENNKLIKIPSGLPKLYLQIFLHNSIARGVNDPCPTVPKMKKSLYSALSIFNNPV 353  
 DB 267 HLGNIKKIKIPSGLPKLYLQIFLHNSIARGVNDPCPTVPKMKKSLYSALSIFNNPV 326  
 QY 354 KYWEMQATFRCVLSRMSVOLGNFGM 379  
 DB 327 KYWEMQATFRCVLSRMSVOLGNFGM 352

RESULT 10

AA895678  
 AA895678 standard; Protein; 246 AA.

XX AA895678;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:18473.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX (HELL-) HELIX RES INST.  
 XX Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX WPI; 2001-318749/34.

DR Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -

XX Claim 8; SEQ ID 18473; 2537pp + CD ROM; English.

PS The present invention describes primer sets for synthesizing 5602  
 XX full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB93893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

XX Sequence 246 AA;

Query Match 62.1%; Score 1237; DB 22; Length 246;  
 Best Local Similarity 96.7%; Pred. No. 5.4e-107;  
 Matches 237; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDT-----DDDDDDDDDDDDDDNSLF 56  
 DB 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDNSLF 60

QY 57 PTREPRSHFFPDLFPMCPFCQCYSRVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEI 116  
 DB 61 PTREPRSHFFPDLFPMCPFCQCYSRVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEI 120

QY 117 KENDFKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSLSEIPLNPKSLAELR 176  
 DB 121 KENDFKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSLSEIPLNPKSLAELR 180

QY 177 THENKVKIKQKDTFGMMALHVLMSANPLDNNNGIEGAFEGVTVFHRIAEAKLTSVPK 236  
 DB 181 THENKVKIKQKDTFGMMALHVLMSANPLDNNNGIEGAFEGVTVFHRIAEAKLTSVPK 240

QY 237 GLPPT 241

DB 241 DNLPS 245

RESULT 11

AA87951  
 ID AA87951 standard; Protein; 369 AA.

XX AA87951;

XX



DT 20-MAR-1996 (first entry)  
 XX Rat neurotrophic biglycan.  
 DE Biglycan; proteoglycan; chondroitin sulphate; neuron protection;  
 XX neurotrophic; central nervous system; CNS; memory loss; dementia;  
 KW learning.  
 KW  
 XX Rattus sp.  
 OS  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..37  
 FT Region /label= Sig\_peptide  
 FT 44..60  
 FT /label= Hypervariable\_region  
 XX WO9530432-A1.  
 XX 16-NOV-1995.  
 XX 09-MAY-1994; 94WO-EP01479.  
 XX 09-MAY-1994; 94WO-EP01479.  
 XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX Hasenoechl R, Huston J, Junghans U, Kappler J, Koops A;  
 PI Mueller HW;  
 XX WPI; 1995-403938/51.  
 DR N-PSDB; AAT08768.  
 XX  
 XX Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s)  
 PT for maintain structural and function of the CNS and attenuating  
 PT memory deficit(s) in the elderly and patients with dementia  
 XX  
 PS Claim 1; Page 44-45; 60pp; English.  
 XX  
 XX Rat biglycan (AAR87951) is a chondroitin sulphate proteoglycan with  
 CC neurotrophic activity for brain neurons. Recombinant biglycan,  
 CC obtd. by expression of encoding cDNA (AAT08768) in eukaryotic host  
 CC cells, can be used to enhance the survival and maintain the structure  
 CC and function of CNS neurons during normal aging as well as after  
 CC pathological and/or traumatic nervous system damage. It can also  
 CC be used to restore function following nervous system lesions and  
 CC degenerative diseases, and to improve learning efficiency and memory  
 CC in the elderly and in patients with dementia.  
 XX  
 XX Sequence 369 AA;  
 SQ

Query Match  
 Best Local Similarity 52.2%; Score 1040.5; DB 16; Length 369;  
 Matches 199; Conservative 67; Mismatches 93; Indels 19; Gaps 3;

QY 4 YVLLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLPFTR 59  
 DB 5 WLLTLLALLSQAPEQKGFWDFTLDDGLLMMNDEERASGDTTSGVPDLD---SLTPT- 59  
 QY 60 EPRSHFFPDLFPMCPFCGCQCYSRVHCSDGLTNSVTNIPFDFRMLDLQNNKIKEIKEN 119  
 DB 60 -----FSAMCPFCGCHLRVQCSDGLTVPKEISPDFTLLDLQNNDISLRKD 109  
 QY 120 DFKGTSLYGLILNNKLTTHPKAFITTKRLRLYLHSHNOLSPILNLPKSLAELRIHE 179  
 DB 110 DFKGLQHLVALVNNKISKIHEKAFSPRLKQKLYISKNHVLEIPNLPSSLVEIRIHD 169  
 QY 180 NKVKIKQDTFGMNAHLVEMSNANPDNNNGIEPAGFEGVTVFHRIAEAKLTSPKGLP 239  
 DB 170 NKIRKVPKGVFSGLRNMNCIEMGNFENSGFEPGADGLKLVLRISAEKLTGIPKLP 229  
 QY 240 PTLLEHLHDYKISTVELEDFKRYKELQRLGLGNKTTIDENGSLANIIPRVRIHLENNK 299  
 DB 230 ETLNELHLDHNKIQAIIELEDLRLSKYLRUGIGHNQIRMIENGSLSLFPLTLRELHLDNNK 289

QY 300 LKIPISGLPELKYLIIFLHSHNSIARVCVNDFTVFKMKKSLYSALSLENNPKYWEWO 359  
 DB 290 LSRVFAGLPDLKLLQVYLLHSHNITKVGINDFCPMGFGYKARAYNGISLFNPNVPYWEVO 349  
 QY 360 PATFRCVLSRMSVOLGNF 377  
 DB 350 PATFRCVTDRLATQFGNY 367

RESULT 12  
 AAB85043  
 ID AAB85043 standard; Protein; 368 AA.  
 XX  
 AC AAB85043;  
 XX  
 DT 06-AUG-2001 (first entry)  
 XX  
 DE Human biglycan protein sequence.  
 XX  
 KW Dystrophin-associated protein complex; DAPC; postsynaptic membrane;  
 KW biglycan; muscular dystrophy; neuromuscular; neurological; smooth muscle;  
 KW nontropic; neuroleptic; antiviral.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200136475-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 17-NOV-2000; 2000WO-US31661.  
 XX  
 PR 18-NOV-1999; 99US-0166253.  
 XX  
 PA (UYBR-) UNIV BROWN RES FOUND.  
 XX  
 PI Fallon J, McKechnie B, Rafii M, Creely H, Bowe M, Ferri R;  
 WPI: 2001-355617/37.  
 DR N-PSDB; AAF83977.  
 XX  
 PT Stabilizing dystrophin-associated protein complexes and activating  
 PT postsynaptic membrane of a cell for treating or preventing muscular,  
 PT neuromuscular and neurological disorders, involves contacting cell with  
 PT biglycan  
 XX  
 PS Disclosure: Page 101-108; 112pp; English.  
 XX  
 CC The invention relates to stabilizing dystrophin-associated protein  
 CC complexes (DAPCs) on the surface of a cell or activating a postsynaptic  
 CC membrane of a cell that comprises contacting the cell with an effective  
 CC amount of biglycan. A composition comprising biglycan or its portion  
 CC is useful for treating or preventing a condition associated with abnormal  
 CC DAPC in cells, characterized by breakdown of muscle cell membrane, which  
 CC includes muscular dystrophies, such as Duchenne's, Becker's, Congenital,  
 CC Limb-girdle muscular dystrophy and myotonic dystrophy and a condition  
 CC characterized by abnormal neuromuscular junction or synapse, such as  
 CC neuromuscular or neurological diseases in a subject. Neurological  
 CC disorders, include polymyositis and Alzheimer's disease. Biglycan is also  
 CC useful for preventing and treating smooth muscle disorders, such as  
 CC cardiac myopathies and for treating and inhibiting infections of cells by  
 CC microorganisms e.g. viruses. Agents that modulate the activity of  
 CC DAG-125, identified by the methods are useful in the prophylactic and  
 CC therapeutic treatments of diseases or disorders, characterized by an  
 CC unstable DAPC or an inappropriate formation of a postsynaptic  
 CC differentiation. Biglycans are also useful as a supplement to brain or  
 CC muscle cell or tissue culture and, tissues can be incubated in vitro  
 CC with biglycan to reverse tissue atrophy and to improve their growth or  
 CC survival in vitro. The present sequence represents the human biglycan.  
 XX  
 SQ Sequence 368 AA;

Query Match 51.9%; Score 1034; DB 22; Length 368;

PS Claim 3; Fig 8; 60pp; English.  
XX Human biglycan (AAR87952) is a chondroitin sulphate proteoglycan with  
CC neurotrophic activity for brain neurons. It can be used to enhance  
CC the survival and maintain the structure and function of CNS neurons  
CC during normal ageing as well as after pathological and/or traumatic  
CC nervous system damage. It can also be used to restore function  
CC following nervous system lesions and degenerative diseases, and to  
CC improve learning efficiency and memory in the elderly and in patients  
CC with dementia.  
XX

SQ Sequence 369 AA:  
Query Match 51.8%; Score 1031.5; DB 16; Length 369;  
Best Local Similarity 52.9%; Pred. No. 1.4e-87;  
Matches 199; Conservative 64; Mismatches 94; Indels 19; Gaps 3;  
QY 6 LLLFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFTPTREP 61  
DB 7 LVSLALALSOALPFQGRFWDFTLDDGPFMMNDEASGADTTSGLVDPD----SVTPYS- 61  
QY 62 RSHFFPDLFPMCPGCGOCYSRVVHCSDGLTTSVPTNIPEDTRMLDQNNKIKKIKENDF 121  
DB 62 RSHFFPDLFPMCPGCGOCYSRVVHCSDGLTTSVPTNIPEDTRMLDQNNKIKKIKENDF 121  
QY 122 KGLTSLYGLILNNKLTIKHPKAFITTKLRRLYLSHNQISEIPNLPKSLAELRIHENK 181  
DB 112 KGLHLYALVLNNKISKIHEKAFSPURKQKLYISKNHVETPPNPSLSVELRIHDNR 171  
QY 182 VKKIQDPTFKGNALHVLMSANPDNNGIEPGAFEGVTVFHRIAEAKLTSPKGLPPT 241  
DB 172 IRKVPKGVFSGLRNMCNENGNPLENSGFEFGADGLKLYLRISEAKLTGIPKDLPET 231  
QY 242 LLELHLDYNKISTVELEDFKRYKELORLGLGNKLTIDENGSLANIPRVREIHLNKKL 301  
DB 232 LNELHLDHKNKIQAELEDLRLYKLYRLGLGHQIRMLIENGSLFSLPTLRELHLDNNKLS 291  
QY 302 KIPSGLPKLYLQIIFLHNSNISTARVGVNDFCTVPKMKKSLYSALSIFNNPVYWEQPA 361  
DB 292 RVPAGLPDLKLLQVYVLSNITKVGNDFCPMGFGVKRAYNGISLNFNNPVYWEQPA 351  
QY 362 TPRCVLSRMSVOLGNF 377  
DB 352 TPRCVTDRLAIOFGNY 367

RESULT 14  
AAG78510  
ID AAG78510 standard; protein; 368 AA.  
XX  
XX  
AC AAG78510;  
XX  
DT 29-JAN-2002 (first entry)  
XX  
XX Human biglycan amino acid sequence.  
XX  
KW Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;  
KW TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic;  
KW Nephrotropic; Antirheumatic; Antiarthritic; Vasotropic; Vulnary  
KW Antiartherosclerotic; Hepatotropic; Cardiac; Dermatological;  
KW Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis;  
KW Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.  
XX  
OS Homo sapiens.  
XX  
XX US6277812-B1.  
XX  
XX 21-AUG-2001.  
XX  
XX 02-JUN-1995; 95US-0458834.  
XX  
XX 14-NOV-1991; 91US-0792192.  
XX  
XX 17-NOV-1992; 92US-0978931.  
PR

Best Local Similarity 53.2%; Pred. No. 8e-88;  
Matches 200; Conservative 63; Mismatches 93; Indels 20; Gaps 3;  
QY 6 LLLFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFTPTREP 61  
DB 7 LVSLALALSOALPFQGRFWDFTLDDGPFMMNDEASGADTTSGLVDPD----SVTPYS- 60  
QY 62 RSHFFPDLFPMCPGCGOCYSRVVHCSDGLTTSVPTNIPEDTRMLDQNNKIKKIKENDF 121  
DB 61 RSHFFPDLFPMCPGCGOCYSRVVHCSDGLTTSVPTNIPEDTRMLDQNNKIKKIKENDF 110  
QY 122 KGLTSLYGLILNNKLTIKHPKAFITTKLRRLYLSHNQISEIPNLPKSLAELRIHENK 181  
DB 111 KGLHLYALVLNNKISKIHEKAFSPURKQKLYISKNHVETPPNPSLSVELRIHDNR 170  
QY 182 VKKIQDPTFKGNALHVLMSANPDNNGIEPGAFEGVTVFHRIAEAKLTSPKGLPPT 241  
DB 171 IRKVPKGVFSGLRNMCNENGNPLENSGFEFGADGLKLYLRISEAKLTGIPKDLPET 230  
QY 242 LLELHLDYNKISTVELEDFKRYKELORLGLGNKLTIDENGSLANIPRVREIHLNKKL 301  
DB 231 LNELHLDHKNKIQAELEDLRLYKLYRLGLGHQIRMLIENGSLFSLPTLRELHLDNNKLA 290  
QY 302 KIPSGLPKLYLQIIFLHNSNISTARVGVNDFCTVPKMKKSLYSALSIFNNPVYWEQPA 361  
DB 291 RVPAGLPDLKLLQVYVLSNITKVGNDFCPMGFGVKRAYNGISLNFNNPVYWEQPA 350  
QY 362 TPRCVLSRMSVOLGNF 377  
DB 351 TPRCVTDRLAIOFGNY 366

RESULT 13  
AAR87952  
ID AAR87952 standard; Protein; 369 AA.  
XX  
XX  
AC AAR87952;  
XX  
DT 20-MAR-1996 (first entry)  
XX  
XX Human neurotrophic biglycan.  
XX  
KW Biglycan; proteoglycan; chondroitin sulphate; neuron protection;  
KW neurotrophic; central nervous system; CNS; memory loss; dementia;  
KW learning.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..37  
XX FT /label= Sig\_peptide  
XX Region 44..60  
XX /label= Hypervariable\_region  
XX  
XX WO9530432-A1.  
XX  
XX 16-NOV-1995.  
XX  
XX 09-MAY-1994; 94WO-EP01479.  
XX  
XX 09-MAY-1994; 94WO-EP01479.  
XX  
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
XX Hasenoehtl R. Huston J. Junghans U. Kappler J. Koops A;  
XX Mueller HW;  
XX  
XX WPI; 1995-403938/51.  
XX  
XX Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s)  
XX for maintain structural and function of the CNS and attenuating  
XX memory deficit(s) in the elderly and patients with dementia  
XX  
XX

PR 08-SEP-1994; 94US-0303238.  
 PR 28-JUN-1988; 88US-0212702.  
 PR 22-JAN-1990; 90US-0467888.  
 PR 13-MAY-1992; 92US-0882345.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PT Ruoslahti EL, Yamaguchi Y;  
 XX  
 DR WPI; 2001-610491/70.  
 XX  
 PT Use of decorin or biglycan polypeptide for inhibiting TGF-beta activity  
 PT in the treatment of dermal wounds and cancer  
 XX  
 PS Example 7; Fig 11; 40pp; English.  
 XX  
 CC The invention relates to the inhibition of transforming growth  
 CC factor-beta (TGF-beta) activity involving contacting TGF-beta with a  
 CC purified polypeptide comprising leucine-rich amino acid sequence of a  
 CC member of decorin superfamily of mammalian proteoglycans. The following  
 CC activities can be attributed to the polypeptide of the invention:  
 CC cytostatic, nephrotropic, antirheumatic, antiarthritic, vasotrophic,  
 CC antiarteriosclerotic, hepatotropic, cardiant, dermatological and  
 CC vulnary. Polypeptides of the invention act as transforming growth  
 CC factor-beta (TGF-beta) binder. The polypeptides of the invention can be  
 CC used for treating a pathology, particularly proliferative pathology  
 CC caused by a transforming growth factor-beta (TGF-beta) regulated  
 CC activity such as cancer; particularly fibrotic cancer, fibrotic  
 CC disease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis,  
 CC adult respiratory distress syndrome, cirrhosis of liver, fibrosis of  
 CC lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty  
 CC restenosis, renal interstitial fibrosis and certain dermal fibrotic  
 CC conditions such as keloids and scarring resulting from burn injuries;  
 CC other invasive skin injuries and reconstructive surgery. The wounds  
 CC treated with the polypeptide, particularly decorin exhibit no detectable  
 CC scarring, and are histologically normal. The current sequence represents  
 CC human biglycan.  
 XX  
 SQ Sequence 368 AA;  
 CC  
 CC Query Match 51.3%; Score 1021; DB 22; Length 368;  
 CC Best Local Similarity 52.4%; Pred. No. 1.3e-86;  
 CC Matches 197; Conservative 64; Mismatches 95; Indels 20; Gaps 3;  
 QY 6 LLLFLALCSAKPF----FSPSHIALKNMMLKMDTDDDDDDDDDDDDNSLFPPTREP 61  
 DQ 7 LVSLALSQLALPFEQGFWDFTLDDGPFMMNDEASGADTSGVLDPD-----SVTPYS- 60  
 QY 62 RSHFFPDLFPMCFGCOCYSRVVHCSDLGLTSVPTNIPDTRMLDQNNKIKEKENDF 121  
 DB 61 -----AMCPFGCHLVRVQCSDGLGKSVPKETSPDPTLLDQNNDISLRKDDF 110  
 QY 122 KGLTSLYGLIANNKLTIKHPKAFITTKLRRLYLSHNQLSEIPLNPKSLAEIRIHENK 181  
 DB 111 KGLHLYALVLVNNKISKIHEKAFSPLRNVQKIYISKNHILVEIPNLSLVELLIHNR 170  
 QY 182 VKKIQKDTFGKMNALHVLMSANPLDNNNGIEPAGFEGVTVFHRIAEAKLTISVPKGLPPT 241  
 DB 171 IRKVPNGVFSGLRNMNCIEMGNPLENSGPEGAFDGLKLNLRISAKLTGPKDLPET 230  
 QY 242 LLELHLDYKISTVELEDFKRYKELQRLGLGNKLTIDTENGSLANIIPRVREIHLNENK 301  
 DB 231 LNELHLDHNKIQAELEDLRLSKYLRGLGHQIRMIENGSLFPLTLRELHLDNNKLA 290  
 QY 302 KIPSGELPKYLIQITFLHSNSTARVGNDFCTVPKMKKSLYSATSLFNNPVKVMOP 361  
 DB 291 RYPSGLPLDKLQVYVLSNNTTKVGNDFCPCMGFVKRAYNGISLNNPVVWEVOP 350  
 QY 362 TFRCVLSRMSVOLGNF 377  
 DB 351 TFRCVTDRLAIQFGNY 366

RESULT 15  
 AAR05159  
 XX AAR05159 standard; protein; 368 AA.  
 XX  
 AC AAR05159;  
 XX  
 DT 17-DEC-2001 (updated)  
 DT 09-OCT-1990 (first entry)  
 XX  
 DE Sequence of human bone proteoglycan I (biglycan).  
 XX  
 KW Osteoporosis; rheumatoid arthritis; Paget's disease;  
 KW atherosclerosis; periodontal; human bone matrix; proteoglycan.  
 XX  
 OS Homo sapiens.  
 XX  
 PN USN7432044-N.  
 XX  
 PD 17-APR-1990.  
 XX  
 PF 03-NOV-1989; 89US-0432044.  
 PR 03-NOV-1989; 89US-0432044.  
 XX (USSH ) NAT INST OF HEALTH.  
 PI Termine J;  
 DR WPI; 1990-178641/23.  
 DR N-PSDB; AAQ04490.  
 XX  
 CC Human bone matrix DNA and proteins -  
 CC used in detection, diagnosis and treatment involving skeletal  
 CC and/or connective tissue disease states.  
 XX  
 PS Disclosure; : p; English.  
 XX  
 CC Probes and Abs raised to the proteins can be used to determine  
 CC their levels useful in diagnosis of associated connective tissue  
 CC diseases states such as osteoporosis, osteo/rheumatoid arthritis,  
 CC Paget's disease, arteriosclerosis and periodontal disease.  
 CC Proteins may also be used to induce or block biological function.  
 CC (Note: Revised entry submitted to correct the patent number format of  
 CC US Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent  
 CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)  
 XX  
 SQ Sequence 368 AA;  
 CC  
 CC Query Match 51.2%; Score 1020; DB 11; Length 368;  
 CC Best Local Similarity 52.1%; Pred. No. 1.6e-86;  
 CC Matches 196; Conservative 66; Mismatches 94; Indels 20; Gaps 3;  
 QY 6 LLLFLALCSAKPF----FSPSHIALKNMMLKMDTDDDDDDDDDDNSLFPPTREP 61  
 DB 7 LVSLALSQLALPFEQGFWDFTLDDGPFMMNDEASGADTSGVLDPD-----SVTPYS- 60  
 QY 62 RSHFFPDLFPMCFGCOCYSRVVHCSDLGLTSVPTNIPDTRMLDQNNKIKEKENDF 121  
 DB 61 -----AMCPFGCHLVRVQCSDGLGKSVPKETSPDPTLLDQNNDISLRKDDF 110  
 QY 122 KGLTSLYGLIANNKLTIKHPKAFITTKLRRLYLSHNQLSEIPLNPKSLAEIRIHENK 181  
 DB 111 KGLHLYALVLVNNKISKIHEKAFSPLRNVQKIYISKNHILVEIPNLSLVELLIHNR 170  
 QY 182 VKKIQKDTFGKMNALHVLMSANPLDNNNGIEPAGFEGVTVFHRIAEAKLTISVPKGLPPT 241  
 DB 171 IRKVPNGVFSGLRNMNCIEMGNPLENSGPEGAFDGLKLNLRISAKLTGPKDLPET 230  
 QY 242 LLELHLDYKISTVELEDFKRYKELQRLGLGNKLTIDTENGSLANIIPRVREIHLNENK 301  
 DB 231 LNELHLDHNKIQAELEDLRLSKYLRGLGHQIRMIENGSLFPLTLRELHLDNNKLA 290



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2003, 16:04:11 ; Search time 23 Seconds  
(without alignments)  
1634.193 Million cells

**Title:** US-09-944-457-2

Perfect score:

Sequence: 1 MKEYVLLFLALCSAKPFFS.....PATFRCVLSRMSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- ```

1: /cgn2_6/ptodata/2/pubbaa/US08_NEW_PUB.pcp.*
2: /cgn2_6/ptodata/2/pubbaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/2/pubbaa/US05_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/2/pubbaa/US06_PUBCOMB.pcp.*
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8: /cgn2_6/ptodata/2/pubbaa/US08_PUBCOMB.pcp.*
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11: /cgn2_6/ptodata/2/pubbaa/US10_NEW_PUB.pcp.*
12: /cgn2_6/ptodata/2/pubbaa/US10_PUBCOMB.pcp.*
13: /cgn2_6/ptodata/2/pubbaa/US60_NEW_PUB.pcp.*
14: /cgn2_6/ptodata/2/pubbaa/US60_PUBCOMB.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query % |     | Length | DB                | ID | Description       |
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| 1          | 1992  | 100.0   | 379 | 9      | US-09-944-413-2   |    | Sequence 2, Appli |
| 2          | 1992  | 100.0   | 379 | 9      | US-09-944-403-2   |    | Sequence 2, Appli |
| 3          | 1992  | 100.0   | 379 | 9      | US-09-944-896-2   |    | Sequence 2, Appli |
| 4          | 1992  | 100.0   | 379 | 9      | US-09-944-944-2   |    | Sequence 2, Appli |
| 5          | 1992  | 100.0   | 379 | 9      | US-09-944-907-2   |    | Sequence 2, Appli |
| 6          | 1992  | 100.0   | 379 | 9      | US-09-944-929-2   |    | Sequence 2, Appli |
| 7          | 1992  | 100.0   | 379 | 9      | US-10-028-072-328 |    | Sequence 328, App |
| 8          | 1992  | 100.0   | 379 | 9      | US-10-121-049-328 |    | Sequence 328, App |
| 9          | 1992  | 100.0   | 379 | 9      | US-10-133-904-328 |    | Sequence 328, App |
| 10         | 1992  | 100.0   | 379 | 9      | US-10-140-470-328 |    | Sequence 328, App |
| 11         | 1992  | 100.0   | 379 | 9      | US-10-175-746-328 |    | Sequence 328, App |
| 12         | 1992  | 100.0   | 379 | 9      | US-10-176-918-328 |    | Sequence 328, App |
| 13         | 1992  | 100.0   | 379 | 9      | US-10-176-921-328 |    | Sequence 328, App |
| 14         | 1992  | 100.0   | 379 | 9      | US-10-137-865-328 |    | Sequence 328, App |
| 15         | 1992  | 100.0   | 379 | 9      | US-10-140-474-328 |    | Sequence 328, App |
| 16         | 1992  | 100.0   | 379 | 9      | US-10-142-431-328 |    | Sequence 328, App |
| 17         | 1992  | 100.0   | 379 | 9      | US-10-143-114-328 |    | Sequence 328, App |
| 18         | 1992  | 100.0   | 379 | 9      | US-10-140-002-328 |    | Sequence 328, App |
| 19         | 1992  | 100.0   | 379 | 9      | US-10-142-419-328 |    | Sequence 328, App |

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61 PRSHFFPDLDFPMCPGCGOCYSRVVHCSDGLTTSVPTNIPFDTMLDLQNNKIKEIKEND 120  
61 PRSHFFPDLDFPMCPGCGOCYSRVVHCSDGLTTSVPTNIPFDTMLDLQNNKIKEIKEND 120  
121 FKGLTSLYGLILNNKLTTHPKAFLTTRKKRLYLHSHNQLSEIPLNPKSLAELRIHEN 180  
121 FKGLTSLYGLILNNKLTTHPKAFLTTRKKRLYLHSHNQLSEIPLNPKSLAELRIHEN 180  
181 KVKKIOTKDFKGMNALHVLMSANPLDNGIEPGAFEGTVFHIRTAFAKLTSPVKGLEPP 240  
181 KVKKIOTKDFKGMNALHVLMSANPLDNGIEPGAFEGTVFHIRTAFAKLTSPVKGLEPP 240  
241 TLLELHLDYNKISTVELEDFKRYKELQRLGNNKLTIDENGLANIPTVRETHLENNKL 300  
241 TLLELHLDYNKISTVELEDFKRYKELQRLGNNKLTIDENGLANIPTVRETHLENNKL 300  
301 KIPSGLPKLYLQIIFLHNSIARVGVNDFCTVPMKMKSLYSALSLFNNPVKYWEMQP 360  
301 KIPSGLPKLYLQIIFLHNSIARVGVNDFCTVPMKMKSLYSALSLFNNPVKYWEMQP 360  
361 ATFCVLSRMSVOLGNEGM 379  
361 ATFCVLSRMSVOLGNEGM 379

Query Match 100.0%; Score 1992; DB 9; Length 379;  
Best Local Similarity 100.0%; Pred. No. 8.6e-159;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKEYVLLFLALCSAKPFPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDNSLFFPTRE 60  
PRIOR APPLICATION NUMBER: 60/069,702  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,870  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/069,873  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/068,017  
PRIOR FILING DATE: December 18, 1997  
PRIOR APPLICATION NUMBER: 60/070,440  
PRIOR FILING DATE: January 5, 1998  
PRIOR APPLICATION NUMBER: 60/074,086  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/074,092  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/075,945  
PRIOR FILING DATE: February 25, 1998  
PRIOR APPLICATION NUMBER: 60/112,850  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 60/113,296  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 60/146,222  
PRIOR FILING DATE: July 28, 1999  
PRIOR APPLICATION NUMBER: PCT/US98/19330  
PRIOR FILING DATE: September 16, 1998  
PRIOR APPLICATION NUMBER: PCT/US98/25108  
PRIOR FILING DATE: December 1, 1998  
PRIOR APPLICATION NUMBER: 09/216,021  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 09/218,517  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 09/254,311  
PRIOR FILING DATE: March 3, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: June 22, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: September 15, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28409  
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28301  
PRIOR FILING DATE: December 1, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: December 16, 1999  
PRIOR APPLICATION NUMBER: PCT/US00/03565  
PRIOR FILING DATE: February 11, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: February 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: March 2, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/08439  
PRIOR FILING DATE: March 30, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: May 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: July 28, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/42678  
PRIOR FILING DATE: December 1, 2000  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: February 28, 2001  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 2  
LENGTH: 379  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-944-413-2

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: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
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: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020165143A1entb
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020165143A1entb
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 2
: LENGTH: 379
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-09-944-403-2

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|    | Query Match           | 100.0%                                                            | Score 1992: | DB 9:      | Length 379; |
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|    | Best Local Similarity | 100.0%;                                                           | Pred. No.   | 8.6e-159;  |             |
|    | Matches 379;          | Conservative                                                      | 0;          | Mismatches | 0; Indels   |
| QY | 1                     | MKEYVLLFLALCSAKPFPSHTALKNMMLKOWETDDDDDDDDDDDDDDDDDDDDDDDDNSLFPFRE | 60          |            |             |
| Dd | 1                     | MKEYVLLFLALCSAKPFPSHTALKNMMLKOWETDDDDDDDDDDDDDDDDDDDDDDDDNSLFPFRE | 60          |            |             |
| QY | 61                    | PRSHFFPDLFPMCFGCQYSRVVHGSDDLGLTSVPNIPFDFTMLDLONNKKIKETEND         | 120         |            |             |

|                                                                           |     |                                                               |     |
|---------------------------------------------------------------------------|-----|---------------------------------------------------------------|-----|
| Db                                                                        | 61  | PRSHFFPDLFPMCPFGCQCYSRVVHCHSCDGLGTSVPTNIPFDTRMLDLQNNKIKETKEND | 120 |
| Qy                                                                        | 121 | FKGLTSLYGLIINNKKLTKIHKRAFTLTKIKRLRLYLSHNSLSEPLNIPKSLAELRTHEN  | 180 |
| Db                                                                        | 121 | FKGLTSLYGLIINNKKLTKIHKRAFTLTKIKRLRLYLSHNSLSEPLNIPKSLAELRTHEN  | 180 |
| Qy                                                                        | 181 | KYKKTKQDTFGKMAHLYLEMSANPLDNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP    | 240 |
| Db                                                                        | 181 | KYKKTKQDTFGKMAHLYLEMSANPLDNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP    | 240 |
| Qy                                                                        | 241 | TLLLEHLDYNKISTVELEDEPKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNNKL   | 300 |
| Db                                                                        | 241 | TLLLEHLDYNKISTVELEDEPKRYKELQRLGLGNKKTIDIEGSLANIPRVREIHLNNKL   | 300 |
| Qy                                                                        | 301 | KKIPSGLPKLYLOIIFLHSNSTIARGVNDPCTVPKMKKSLYSAISLFNPNPKYVEMQP    | 360 |
| Db                                                                        | 301 | KKIPSGLPKLYLOIIFLHSNSTIARGVNDPCTVPKMKKSLYSAISLFNPNPKYVEMQP    | 360 |
| Qy                                                                        | 361 | ATFCVLSRMSVOLGNFGM                                            | 379 |
| Db                                                                        | 361 | ATFCVLSRMSVOLGNFGM                                            | 379 |
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| US-09-944-896-2                                                           |     |                                                               |     |
| : Sequence 2, Application US/09944896                                     |     |                                                               |     |
| : Patent No. US20020168715A1                                              |     |                                                               |     |
| : GENERAL INFORMATION:                                                    |     |                                                               |     |
| : APPLICANT: Baker, Kevin                                                 |     |                                                               |     |
| : APPLICANT: Botstein, David                                              |     |                                                               |     |
| : APPLICANT: Eaton, Dan                                                   |     |                                                               |     |
| : APPLICANT: Ferrara, Napoleone                                           |     |                                                               |     |
| : APPLICANT: Filvaroff, Ellen                                             |     |                                                               |     |
| : APPLICANT: Gerritsen, Mary                                              |     |                                                               |     |
| : APPLICANT: Goddard, Audrey                                              |     |                                                               |     |
| : APPLICANT: Godowski, Paul                                               |     |                                                               |     |
| : APPLICANT: Grimaldi, Christopher                                        |     |                                                               |     |
| : APPLICANT: Gurney, Austin                                               |     |                                                               |     |
| : APPLICANT: Hillan, Kenneth                                              |     |                                                               |     |
| : APPLICANT: Kljavin, Ivar                                                |     |                                                               |     |
| : APPLICANT: Napier, Mary                                                 |     |                                                               |     |
| : APPLICANT: Roy, Margaret                                                |     |                                                               |     |
| : APPLICANT: Tumas, Daniel                                                |     |                                                               |     |
| : APPLICANT: Wood, William                                                |     |                                                               |     |
| : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC |     |                                                               |     |
| : TITLE OF INVENTION: ACIDS ENCODING THE SAME                             |     |                                                               |     |
| : FILE REFERENCE: P2548P1C1                                               |     |                                                               |     |
| : CURRENT APPLICATION NUMBER: US/09/944,896                               |     |                                                               |     |
| : CURRENT FILING DATE: 2001-08-31                                         |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 09/866,028                                    |     |                                                               |     |
| : PRIOR FILING DATE: 2001-05-25                                           |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,334                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 11, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,335                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 11, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,278                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 11, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,425                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 12, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,696                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 16, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,694                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 16, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,702                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 16, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,870                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 17, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/069,873                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 17, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/068,017                                    |     |                                                               |     |
| : PRIOR FILING DATE: December 18, 1997                                    |     |                                                               |     |
| : PRIOR APPLICATION NUMBER: 60/070,440                                    |     |                                                               |     |
| : PRIOR FILING DATE: January 5, 1998                                      |     |                                                               |     |

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PRIOR APPLICATION NUMBER: 60/074.086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074.092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075.945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112.850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113.296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146.222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216.021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218.517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254.311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRI
ORGANISM: Homo Sapien
US-09-944-896-2

Query Match      100.0%; Score 1992; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 8 6e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps

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DB          1 MKXYVLLFLALCSAKPFTSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60

QY         61 PRSHFFPDLPMPGCCOCYSRVVHCSDGLGTSVPNTIPDTRMLDLQNKKIKEIKEND 120
DB         61 PRSHFFPDLPMPGCCOCYSRVVHCSDGLGTSVPNTIPDTRMLDLQNKKIKEIKEND 120

QY        121 PKGITSYGITLNANNKITKHKAFLTTKKLRRLYLSHNOISEIPLNPKSLAELEIHEN 180
DB        121 PKGITSYGITLNANNKITKHKAFLTTKKLRRLYLSHNOISEIPLNPKSLAELEIHEN 180
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Db 301 KAIIPSGLPKYLQIIFLHNSIARVGVNDFCPVPMKKSLYSALISLFNNPVKYWQ 360

QY 361 ATRCVLSRMSVOLGNFGM 379

Db 361 ATRCVLSRMSVOLGNFGM 379

RESULT 6

US-09-944-929-2

Sequence 2, Application US/09944929

Publication No. US20020197612A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kljavin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944, 929

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/866, 028

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 2

LENGTH: 379

TYPE: PRT

ORGANISM: Homo Sapien

US-09-944-929-2

Query Match 100.0%; Score 1992; DB 9; Length 379;

Best Local Similarity 100.0%; Pred. No. 8.6e-159;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLPPTRE 60

Db 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLPPTRE 60

61 PRSHFFPDLFPMCPFCOCYRVVHCSDLGLTSVPTNIPDFTRMLDLQNNKIKETKEND 120

Db 61 PRSHFFPDLFPMCPFCOCYRVVHCSDLGLTSVPTNIPDFTRMLDLQNNKIKETKEND 120

QY 121 FKGLTSYGLTLNKKTKTHPKAFLTKKRLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180

Db 121 FKGLTSYGLTLNKKTKTHPKAFLTKKRLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180

QY 181 KVKTKQDTFGKMHVLEMSANPLDNGIEPCAGVGVTVFHRIAEAKLTSVPKGLPP 240

Db 181 KVKTKQDTFGKMHVLEMSANPLDNGIEPCAGVGVTVFHRIAEAKLTSVPKGLPP 240

QY 241 TLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKTTDIENGSLANIPRVREIHLNNKL 300

Db 241 TLEHLHDYNNKISTVELEDFKRYKELQRLGLGNNKTTDIENGSLANIPRVREIHLNNKL 300

QY 301 KKIFSGLPKYLQIIFLHNSIARVGVNDFCPVPMKKSLYSALISLFNNPVKYWQ 360

Db 301 KKIFSGLPKYLQIIFLHNSIARVGVNDFCPVPMKKSLYSALISLFNNPVKYWQ 360

QY 361 ATRCVLSRMSVOLGNFGM 379

Db 361 ATRCVLSRMSVOLGNFGM 379

RESULT 7

US-10-028-072-328

Sequence 328, Application US/10028072

Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028, 072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059836

PRIOR FILING DATE: 1997-09-24

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062285

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062814

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/062816

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063082

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/063127

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063327

PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063329

PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063550

PRIOR FILING DATE: 1997-10-28

|   |                           |            |
|---|---------------------------|------------|
| ; | PRIOR FILING DATE:        | 1998-05-07 |
| ; | PRIOR APPLICATION NUMBER: | 60/084627  |
| ; | PRIOR FILING DATE:        | 1998-05-07 |
| ; | PRIOR APPLICATION NUMBER: | 60/084637  |
| ; | PRIOR FILING DATE:        | 1998-05-07 |
| ; | PRIOR APPLICATION NUMBER: | 60/085149  |
| ; | PRIOR FILING DATE:        | 1998-05-12 |
| ; | PRIOR APPLICATION NUMBER: | 60/085323  |
| ; | PRIOR FILING DATE:        | 1998-05-13 |
| ; | PRIOR APPLICATION NUMBER: | 60/085338  |
| ; | PRIOR FILING DATE:        | 1998-05-13 |
| ; | PRIOR APPLICATION NUMBER: | 60/085339  |
| ; | PRIOR FILING DATE:        | 1998-05-13 |
| ; | PRIOR APPLICATION NUMBER: | 60/085579  |
| ; | PRIOR FILING DATE:        | 1998-05-15 |
| ; | PRIOR APPLICATION NUMBER: | 60/085697  |
| ; | PRIOR FILING DATE:        | 1998-05-15 |
| ; | PRIOR APPLICATION NUMBER: | 60/085704  |
| ; | PRIOR FILING DATE:        | 1998-05-15 |
| ; | PRIOR APPLICATION NUMBER: | 60/086414  |
| ; | PRIOR FILING DATE:        | 1998-05-22 |
| ; | PRIOR APPLICATION NUMBER: | 60/086430  |
| ; | PRIOR FILING DATE:        | 1998-05-22 |
| ; | PRIOR APPLICATION NUMBER: | 60/087106  |
| ; | PRIOR FILING DATE:        | 1998-05-28 |
| ; | PRIOR APPLICATION NUMBER: | 60/088026  |
| ; | PRIOR FILING DATE:        | 1998-06-04 |
| ; | PRIOR APPLICATION NUMBER: | 60/088730  |
| ; | PRIOR FILING DATE:        | 1998-06-10 |
| ; | PRIOR APPLICATION NUMBER: | 60/088741  |
| ; | PRIOR FILING DATE:        | 1998-06-10 |
| ; | PRIOR APPLICATION NUMBER: | 60/088810  |
| ; | PRIOR FILING DATE:        | 1998-06-10 |
| ; | PRIOR APPLICATION NUMBER: | 60/088858  |
| ; | PRIOR FILING DATE:        | 1998-06-11 |
| ; | PRIOR APPLICATION NUMBER: | 60/089532  |
| ; | PRIOR FILING DATE:        | 1998-06-17 |
| ; | PRIOR APPLICATION NUMBER: | 60/089599  |
| ; | PRIOR FILING DATE:        | 1998-06-17 |
| ; | PRIOR APPLICATION NUMBER: | 60/089907  |
| ; | PRIOR FILING DATE:        | 1998-06-18 |
| ; | PRIOR APPLICATION NUMBER: | 60/089947  |
| ; | PRIOR FILING DATE:        | 1998-06-19 |
| ; | PRIOR APPLICATION NUMBER: | 60/090349  |
| ; | PRIOR FILING DATE:        | 1998-06-23 |
| ; | PRIOR APPLICATION NUMBER: | 60/090429  |
| ; | PRIOR FILING DATE:        | 1998-06-24 |
| ; | PRIOR APPLICATION NUMBER: | 60/090445  |
| ; | PRIOR FILING DATE:        | 1998-06-24 |
| ; | PRIOR APPLICATION NUMBER: | 60/090538  |
| ; | PRIOR FILING DATE:        | 1998-06-24 |
| ; | PRIOR APPLICATION NUMBER: | 60/090863  |
| ; | PRIOR FILING DATE:        | 1998-06-26 |
| ; | PRIOR APPLICATION NUMBER: | 60/091360  |
| ; | PRIOR FILING DATE:        | 1998-07-01 |
| ; | PRIOR APPLICATION NUMBER: | 60/091519  |
| ; | PRIOR FILING DATE:        | 1998-07-02 |
| ; | PRIOR APPLICATION NUMBER: | 60/091982  |
| ; | PRIOR FILING DATE:        | 1998-07-02 |

0.

|    |     |                                                             |     |
|----|-----|-------------------------------------------------------------|-----|
| QY | 1   | MREYVLLFLALCSAKPFPSHIALKNMMLKDMETDDDDDDDDDDDDDDDDDDNSLFP    | 60  |
| DB | 1   | MREYVLLFLALCSAKPFPSHIALKNMMLKDMETDDDDDDDDDDDDDDDDDDNSLFP    | 60  |
| QY | 61  | PRSHFFFDLPMCPGCGCYSRVVHCSDLGTSVPTNIPFTRMLDLQNNKIKETKEND     | 120 |
| DB | 61  | PRSHFFFDLPMCPGCGCYSRVVHCSDLGTSVPTNIPFTRMLDLQNNKIKETKEND     | 120 |
| QY | 121 | FKGLTSLYGLILNNKRLTKIHFKAFLLTTKKLRRLYLHSHNLSLEIPLNLPKSLAEIRI | 180 |

Db 121 FKGTSLYGLTNNKLTTHPKAFLLTKLRRLYLHSHNQLSEIPLNPKSLAEALRIHEN 180  
QY 181 KVKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPP 240  
Db 191 KVKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPP 240  
QY 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKL 300  
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKL 300  
QY 301 KIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSFLNPNVKYEMQP 360  
Db 301 KIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSFLNPNVKYEMQP 360  
QY 361 ATFCVLSRMSVOLGNFGM 379  
Db 361 ATFCVLSRMSVOLGNFGM 379

## RESULT 8

US-10-121-049-328

Sequence 328, Application US/10121049

Publication No. US2003002239A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330RIC17  
; CURRENT APPLICATION NUMBER: US/10/121.049  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 328  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-121-049-328

Query Match 100.0%; Score 1992; DB 9; Length 379;  
Best Local Similarity 100.0%; Pred. No. 8.6e-159;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPPTRE 60  
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPPTRE 60  
QY 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
Db 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
QY 121 FKGLTSLYGLILNNKLTTHPKAFLLTKLRRLYLHSHNQLSEIPLNPKSLAEALRIHEN 180  
Db 121 FKGLTSLYGLILNNKLTTHPKAFLLTKLRRLYLHSHNQLSEIPLNPKSLAEALRIHEN 180  
QY 181 KVKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPP 240  
Db 181 KVKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPP 240

Db 181 KVKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPP 240  
QY 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKL 300  
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKL 300  
QY 301 KIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSFLNPNVKYEMQP 360  
Db 301 KIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSFLNPNVKYEMQP 360  
QY 361 ATFCVLSRMSVOLGNFGM 379  
Db 361 ATFCVLSRMSVOLGNFGM 379

## RESULT 9

US-10-123-904-328

Sequence 328, Application US/10123904

Publication No. US20030022328A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330RIC54  
; CURRENT APPLICATION NUMBER: US/10/123.904  
; CURRENT FILING DATE: 2002-04-16  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 328  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-123-904-328

Query Match 100.0%; Score 1992; DB 9; Length 379;  
Best Local Similarity 100.0%; Pred. No. 8.6e-159;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPPTRE 60  
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDSDNSLFPPTRE 60  
QY 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
Db 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120  
QY 121 FKGLTSLYGLILNNKLTTHPKAFLLTKLRRLYLHSHNQLSEIPLNPKSLAEALRIHEN 180  
Db 121 FKGLTSLYGLILNNKLTTHPKAFLLTKLRRLYLHSHNQLSEIPLNPKSLAEALRIHEN 180  
QY 181 KVKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPP 240  
Db 181 KVKKIQKDTFKGMNALHVLMSANPLDNGIEPGAFEGVTVFHRIAEAKLTSPVKGLPP 240  
QY 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKL 300  
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTDIENGSLANIPRVREIHLNENKL 300

|    |     |                 |               |                 |             |     |
|----|-----|-----------------|---------------|-----------------|-------------|-----|
| Qy | 301 | KKIPSGLPKLYLQII | FLHNSIARVGVND | FCTVPKMKSLYSALS | LFNNPKYWMQP | 360 |
|    |     |                 |               |                 |             |     |
| Db | 301 | KKIPSGLPKLYLQII | FLHNSIARVGVND | FCTVPKMKSLYSALS | LFNNPKYWMQP | 360 |
|    |     |                 |               |                 |             |     |
| Qy | 361 | ATFCVLRSMSV     | LGNGFM        | 379             |             |     |
|    |     |                 |               |                 |             |     |
| Db | 361 | ATFCVLRSMSV     | LGNGFM        | 379             |             |     |
|    |     |                 |               |                 |             |     |

RESULT 10  
US-10-140-470-328  
; Sequence 328, Application US/10140470  
; Publication No. US20030022331A1

|            |                     |
|------------|---------------------|
| APPLICANT: | Baker, Kevin P.     |
| APPLICANT: | Beresini, Maureen   |
| APPLICANT: | DeRose, Laura       |
| APPLICANT: | Desnoyers, Luc      |
| APPLICANT: | Filvaroff, Ellen    |
| APPLICANT: | Gao, Wei-Qiang      |
| APPLICANT: | Garttisen, Mary E.  |
| APPLICANT: | Goddard, Audrey     |
| APPLICANT: | Godowski, Paul J.   |
| APPLICANT: | Gurney, Austin L.   |
| APPLICANT: | Sherwood, Steven    |
| APPLICANT: | Smith, Victoria     |
| APPLICANT: | Stewart, Timothy A. |
| APPLICANT: | Tumas, Daniel       |
| APPLICANT: | Watanabe, Colin K   |
| APPLICANT: | Wood, William       |
| APPLICANT: | Zhang, Zemin        |

```

: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
:
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
:
: FILE REFERENCE: P3330R1C160
:
: CURRENT APPLICATION NUMBER: US/10/140,470
:
: CURRENT FILING DATE: 2002-05-06
:
: Prior Application removed - See Palm or File wrapper
:
: NUMBER OF SEQ ID NOS: 550
:
: SEQ ID NO 328
:
: LENGTH: 379

```

```

;
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-328

```

Query Match 100.0%; Score 1992: DB 9; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-159;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDEDNSLPTRE   60
        |||||
Db      1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDEDNSLPTRE   60
```

[illegible]

|     |                   |         |    |       |     |      |      |      |        |       |     |
|-----|-------------------|---------|----|-------|-----|------|------|------|--------|-------|-----|
| 121 | FKGLTSLYGLILNNKLT | KIHPKAF | LT | TKKLR | LYI | SHNQ | LSEI | PLNP | PKSLAE | RIHEN | 180 |
|     |                   |         |    |       |     |      |      |      |        |       |     |
| 121 | FKGLTSLYGLILNNKLT | KIHPKAF | LT | TKKLR | LYI | SHNQ | LSEI | PLNP | PKSLAE | RIHEN | 180 |

181 KVKKIQKDTFKGMNALHVEMSANPLDNNGIEPGAEGVTVEHRIATAKLTSPVKGLPP 240  
 |||||  
 181 KVKKIQKDTFKGMNALHVEMSANPLDNNGIEPGAEGVTVEHRIATAKLTSPVKGLPP 240  
 |||||

|    |     |        |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |
|----|-----|--------|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|
| QY | 241 | TLLEHL | DY | NK | I | S | T | V | E | L | E | D | F | K | R | Y | K | E | L | Q | R | L | G | N | K | I | T | D | I | E | N | G | S | L | A | N | I | P | R | V | R | E | I | H | L | E | N | K | L | 300 |
|    |     |        |    |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |
| Db | 241 | TLLEHL | DY | NK | I | S | T | V | E | L | E | D | F | K | R | Y | K | E | L | Q | R | L | G | N | K | I | T | D | I | E | N | G | S | L | A | N | I | P | R | V | R | E | I | H | L | E | N | K | L | 300 |

301 KKIPSGLPKYLQIIFLHSNSTARVGVDNFCPTVPKMKKSLYSAISLFNNPKYWEMQP 360  
 |||||  
 301 KKIPSGLPKYLQIIFLHSNSTARVGVDNFCPTVPKMKKSLYSAISLFNNPKYWEMQP 360  
 |||||

---

QY 361 ATERCVLSRMSVQLGNFGM 379  
 |||||  
 Db 361 ATERCVLSRMSVQLGNFGM 379

RESULT 11  
US-10-175-746-328  
; Sequence 328, Application US/10175746  
; Publication No. US20030027270A1

|                      |                     |
|----------------------|---------------------|
| GENERAL INFORMATION: | Baker, Kevin P.     |
| APPLICANT:           | Beresini, Maureen   |
| APPLICANT:           | Desjoeys, Laura     |
| APPLICANT:           | Desnoyers, Luc      |
| APPLICANT:           | Filvaroff, Ellen    |
| APPLICANT:           | Gao, Wei-Qiang      |
| APPLICANT:           | Gerritsen, Mary E.  |
| APPLICANT:           | Goddard, Audrey     |
| APPLICANT:           | Godowski, Paul J.   |
| APPLICANT:           | Gurney, Austin L.   |
| APPLICANT:           | Shorwood, Steven    |
| APPLICANT:           | Smith, Victoria     |
| APPLICANT:           | Stewart, Timothy A. |
| APPLICANT:           | Tumas, Daniel       |
| APPLICANT:           | Watanabe, Colin K.  |
| APPLICANT:           | Wood, William       |
| APPLICANT:           | Zhang, Zemin        |

```

: REFERENCE: zhang, zhang
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330RIC353
: CURRENT APPLICATION NUMBER: US/10/175,746
: CURRENT FILING DATE: 2002-06-19
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
:

```

```

; SEQ ID NO 328
; LENGTH: 379

```

```

; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-328

```

|                       |                 |                     |          |             |
|-----------------------|-----------------|---------------------|----------|-------------|
| Query Match           | 100.0%;         | Score 1992;         | DB 9;    | Length 379; |
| Best Local Similarity | 100.0%;         | Pred. No. 8.6e-159; |          |             |
| Matches 379:          | Conservative 0; | Mismatches 0;       | Indels 0 |             |

```

Qy 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDWEDTDDDDDDDDDDDEDNSLFTRE 60
    |||||
Db 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDWEDTDDDDDDDDDDDEDNSLFTRE 60
    |||||

```

|    |    |                                                          |     |
|----|----|----------------------------------------------------------|-----|
| Qy | 61 | PRSHFFEDLFMCPFGCQCYSRVVHCSDLGLTSVPTNIPFTRMLDQNKKIKEIKEND | 120 |
| Db | 61 | PRSHFFEDLFMCPFGCQCYSRVVHCSDLGLTSVPTNIPFTRMLDQNKKIKEIKEND | 120 |

|    |     |                   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |  |
|----|-----|-------------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|--|
| QY | 121 | FKGLTSLYGLILNNKLT | K | I | H | P | K | A | F | L | T | T | K | L | R | R | L | Y | S | H | N | Q | L | S | E | I | P | I | N | L | P | K | S | L | A | E | L | R | I | H | E | N | 180 |  |
|    |     |                   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |  |
| Db | 121 | FKGLTSLYGLILNNKLT | K | I | H | P | K | A | F | L | T | T | K | L | R | R | L | Y | S | H | N | Q | L | S | E | I | P | I | N | L | P | K | S | L | A | E | L | R | I | H | E | N | 180 |  |

| Accession | Protein                                                         | Length | Score | E-value  | Ident | Positives | Negatives | Score | E-value  | Ident | Positives | Negatives |
|-----------|-----------------------------------------------------------------|--------|-------|----------|-------|-----------|-----------|-------|----------|-------|-----------|-----------|
| QY        | 181 KVKKIQDKDTFGKGNALHVEMSANPLDNNCEPGAFEGVTVFHIRIAEAKLTSVPKGLPP | 240    | 1.0   | 0.000000 | 100   | 100       | 0         | 1.0   | 0.000000 | 100   | 100       | 0         |
| Db        | 181 KVKKIQDKDTFGKGNALHVEMSANPLDNNCEPGAFEGVTVFHIRIAEAKLTSVPKGLPP | 240    | 1.0   | 0.000000 | 100   | 100       | 0         | 1.0   | 0.000000 | 100   | 100       | 0         |

|    |     |          |         |        |        |        |        |        |       |      |     |
|----|-----|----------|---------|--------|--------|--------|--------|--------|-------|------|-----|
| Qy | 241 | TLELHLDY | NKISTVE | EDFKYK | ELQRLG | NNKITT | DIENGL | ANIPRV | REIHL | NNKL | 300 |
|    |     |          |         |        |        |        |        |        |       |      |     |
| Db | 241 | TLELHLDY | NKISTVE | EDFKYK | ELQRLG | NNKITT | DIENGL | ANIPRV | REIHL | NNKL | 300 |

|     |     |                                                            |     |
|-----|-----|------------------------------------------------------------|-----|
| QY  | 301 | KKIPSLPELKYLOIIFLHSNSTARVGNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP | 360 |
|     |     |                                                            |     |
| Ddb | 301 | KKIPSLPELKYLOIIFLHSNSTARVGNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP | 360 |

**Qy**            361 ATFRCVLSRMSVQLGNFGM 379  
             | | | | | | | | | | | | | | | |  
**Db**            361 ATFRCVLSRMSVOLGNFGM 379

## RESULT 12

US-10-176-918-328  
; Sequence 328, Application US/10176918  
; Publication No. US20030027275A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C382  
; CURRENT APPLICATION NUMBER: US/10/176,918  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 328  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-918-328

Query Match 100.0%; Score 1992; DB 9; Length 379;  
Best Local Similarity 100.0%; Pred. No. 8.6e-159;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDNSLFPPTRE 60  
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPPTRE 60  
Qy 61 PRSHFFPDLFPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEIKEND 120  
Db 61 PRSHFFPDLFPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEIKEND 120  
Qy 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNQSLSEIPLNPKSLAELRIHEN 180  
Db 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNQSLSEIPLNPKSLAELRIHEN 180  
Qy 181 KVKKIQKDTFGMNAHVLEMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240  
Db 181 KVKKIQKDTFGMNAHVLEMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240  
Qy 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNNKL 300  
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNNKL 300  
Qy 301 KKIPSGLPKLYLOIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSFLNPNVYWMOP 360  
Db 301 KKIPSGLPKLYLOIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSFLNPNVYWMOP 360  
Qy 361 ATFCVLSRMSVQLGNFGM 379  
Db 361 ATFCVLSRMSVQLGNFGM 379

## RESULT 13

US-10-176-921-328  
; Sequence 328, Application US/10176921  
; Publication No. US20030027276A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C288  
; CURRENT APPLICATION NUMBER: US/10/176,921  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 328  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-921-328

Query Match 100.0%; Score 1992; DB 9; Length 379;  
Best Local Similarity 100.0%; Pred. No. 8.6e-159;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPPTRE 60  
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPPTRE 60  
Qy 61 PRSHFFPDLFPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEIKEND 120  
Db 61 PRSHFFPDLFPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEIKEND 120  
Qy 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNQSLSEIPLNPKSLAELRIHEN 180  
Db 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNQSLSEIPLNPKSLAELRIHEN 180  
Qy 181 KVKKIQKDTFGMNAHVLEMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240  
Db 181 KVKKIQKDTFGMNAHVLEMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240  
Qy 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNNKL 300  
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNNKL 300  
Qy 301 KKIPSGLPKLYLOIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSFLNPNVYWMOP 360  
Db 301 KKIPSGLPKLYLOIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSFLNPNVYWMOP 360  
Qy 361 ATFCVLSRMSVQLGNFGM 379  
Db 361 ATFCVLSRMSVQLGNFGM 379

## RESULT 14

US-10-137-865-328  
; Sequence 328, Application US/10137865  
; Publication No. US20030032155A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen

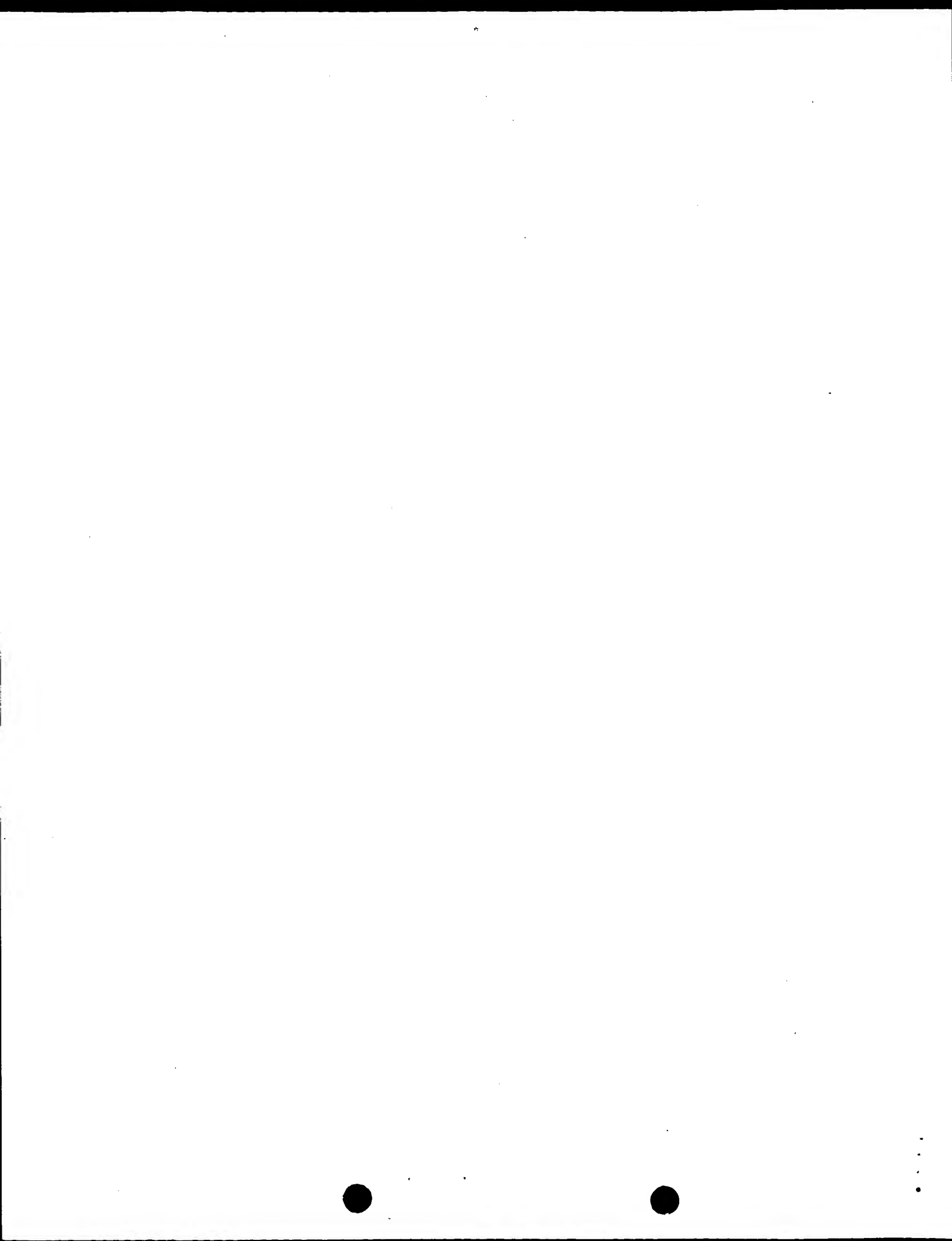
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R01C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 328
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-865-328

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|                       |                 |                                                            |           |             |
|-----------------------|-----------------|------------------------------------------------------------|-----------|-------------|
| Query Match           | 100.0%;         | Score 1992;                                                | DB 9;     | Length 379; |
| Best Local Similarity | 100.0%;         | Pred. No. 8.6e-159;                                        |           |             |
| Matches 379;          | Conservative 0; | Mismatches 0;                                              | Indels 0; | Gaps 0;     |
| QY                    | 1               | MREYVLLFLALCSAKPFPSHIALKNMMLKOWEDTDDDDDDDDDDDDDDNSLFPTR    | 60        |             |
| Db                    | 1               | MREYVLLFLALCSAKPFPSHIALKNMMLKOWEDTDDDDDDDDDDDDDDNSLFPTR    | 60        |             |
| QY                    | 61              | PRSHFFPDLPMCPFGCQCSRVVHCHSDGLTSPVTNIPFTRMLDLONNKIKETKND    | 120       |             |
| Db                    | 61              | PRSHFFPDLPMCPFGCQCSRVVHCHSDGLTSPVTNIPFTRMLDLONNKIKETKND    | 120       |             |
| QY                    | 121             | FKGLTSLYGLILNNKLTKIHPKAFLTTKLRLRYLSHNQSLSEIPLNPKSLAELRIHEN | 180       |             |
| Db                    | 121             | FKGLTSLYGLILNNKLTKIHPKAFLTTKLRLRYLSHNQSLSEIPLNPKSLAELRIHEN | 180       |             |
| QY                    | 181             | KVKTKLOKTFKGMNALHVLMSANPLDNNGIEPGAEGVTVHRIATAEAKLSVPGKLPP  | 240       |             |
| Db                    | 181             | KVKTKLOKTFKGMNALHVLMSANPLDNNGIEPGAEGVTVHRIATAEAKLSVPGKLPP  | 240       |             |
| QY                    | 241             | TLELHLHDYNIKISTVELEDFKRYKELQRLGLGNKTKTDIENGSLANIPRVRIHLENK | 300       |             |
| Db                    | 241             | TLELHLHDYNIKISTVELEDFKRYKELQRLGLGNKTKTDIENGSLANIPRVRIHLENK | 300       |             |
| QY                    | 301             | KKIPSGLPKLYQIIIFLHNSNARVCVDFCTVPKMKKLSYSAISLFPNNPKYWEQ     | 360       |             |
| Db                    | 301             | KKIPSGLPKLYQIIIFLHNSNARVCVDFCTVPKMKKLSYSAISLFPNNPKYWEQ     | 360       |             |

RESULT 15  
US-10-140-474-328  
; Sequence 328, Application US/10140474  
; Publication No. US20030032156A1  
; GENERAL INFORMATION:  
; APPLICANT: Baket, Kevin P.  
; APPLICANT: Bersini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Cao Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.





94964

From:

Sent:

To:

Subject:

Li, Ruixiang  
Friday, May 23, 2003 1:46 PM  
STIC-Biotech/ChemLib  
Sequence search of Application NO: 09/944,457

Please do:

(i) a standard search on SEQ ID NO: 2 against commercial amino acid databases;

(ii) a standard search on SEQ ID NO: 2 against pending interference amino acid databases, print out the summary table only, with 500 hits and no alignments.

Thank you very much!

Ruixiang Li  
GAU 1646  
CM1 10E18  
Mail Box 10D19  
306-0282

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH: \_\_\_\_\_  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.) \_\_\_\_\_  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

